

FIG. 1A

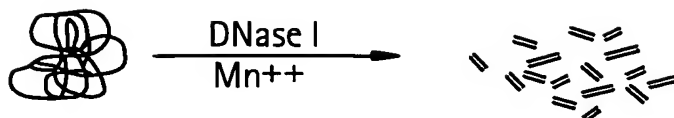


FIG. 1B

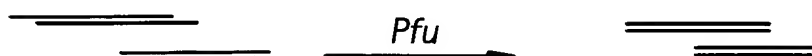


FIG. 1C

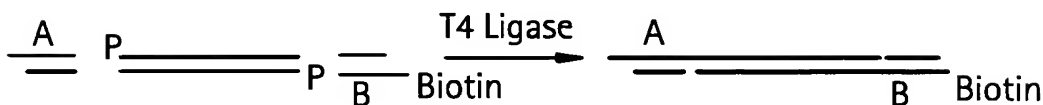


FIG. 1D

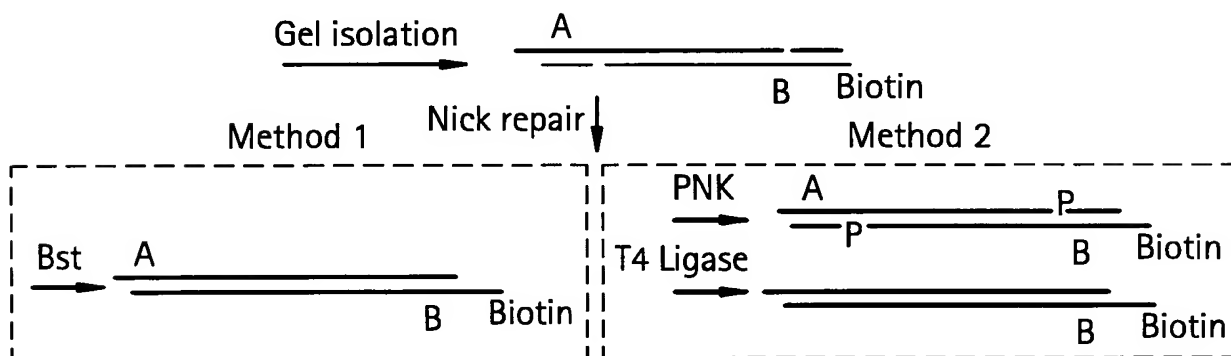


FIG. 1E

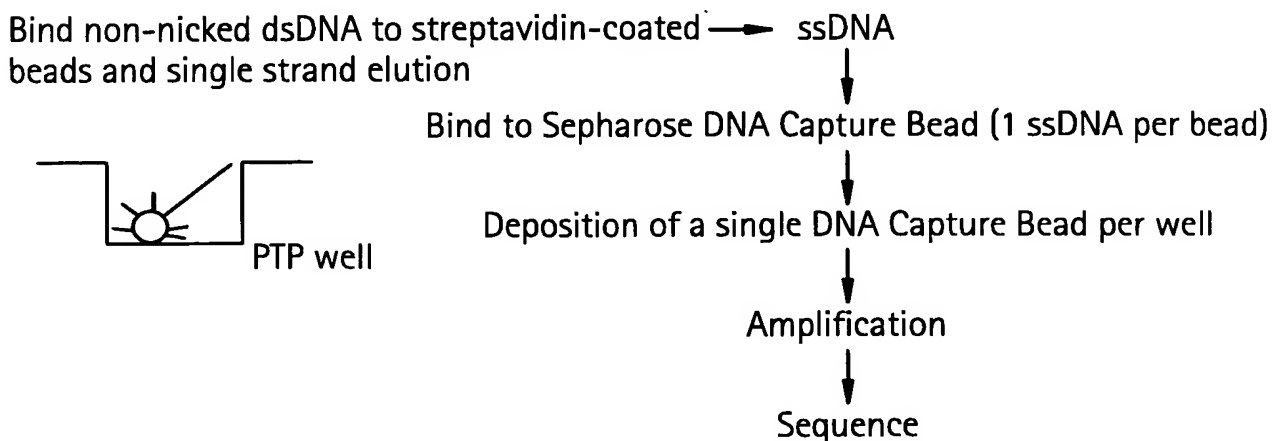


FIG. 1F

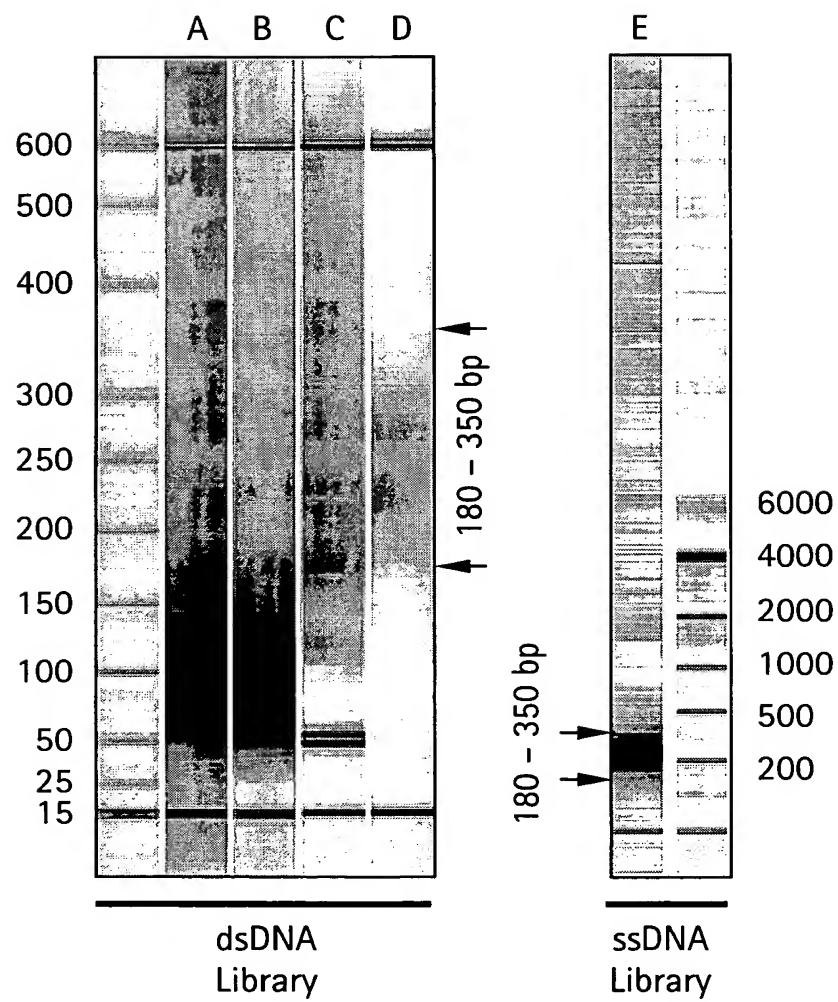


FIG. 1G

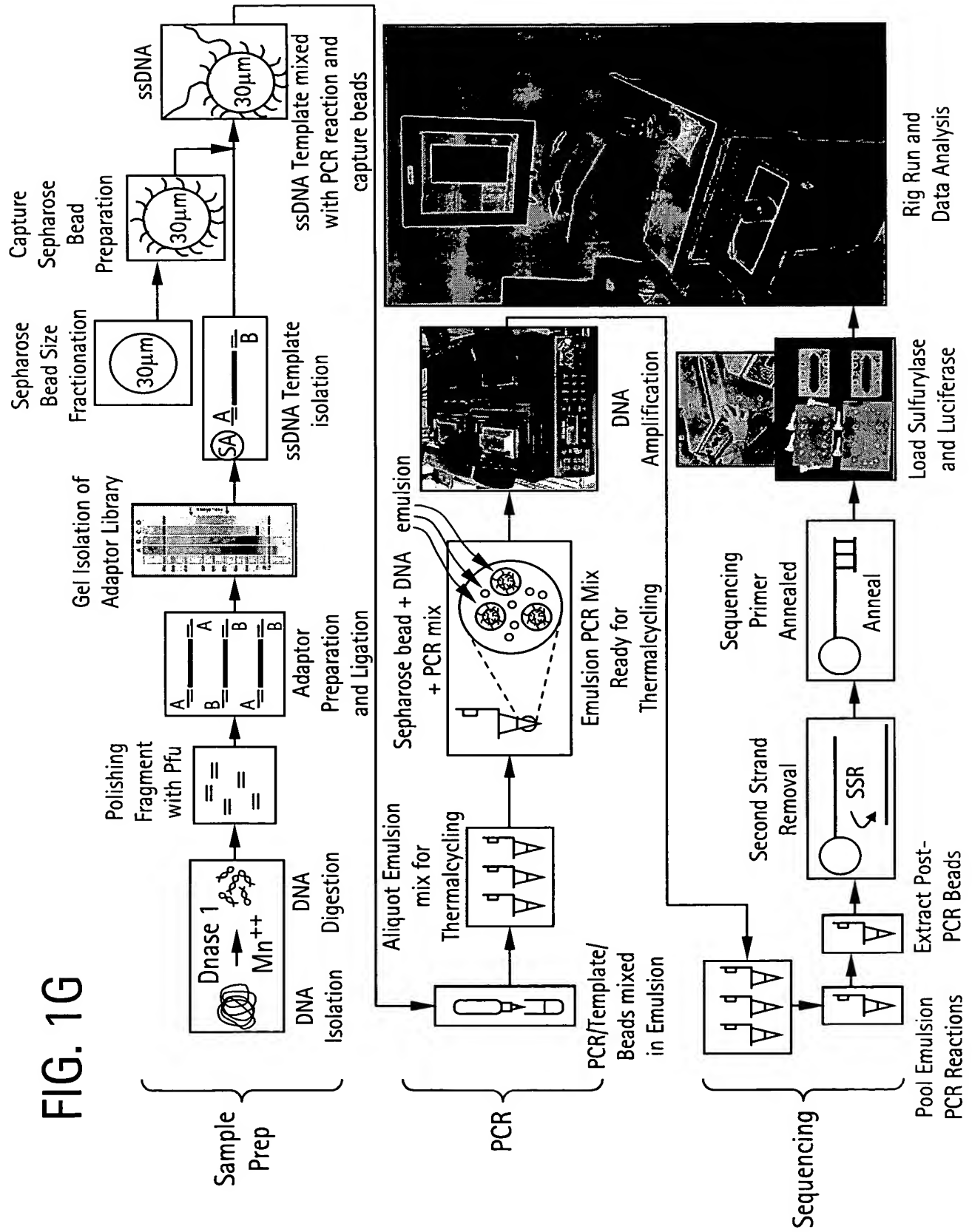


FIG. 2A

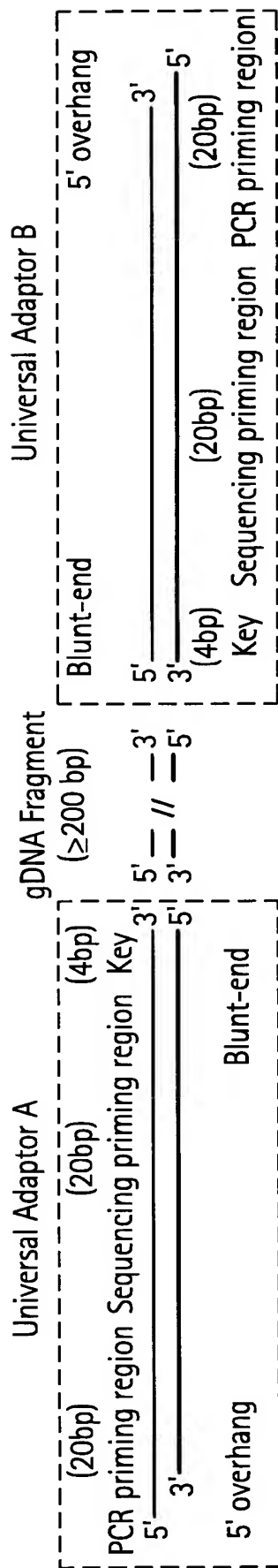


FIG. 2B

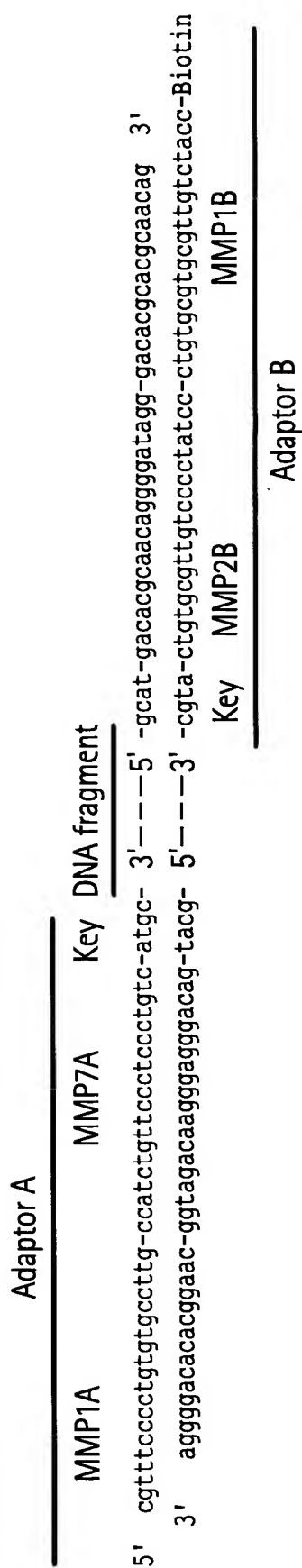


FIG. 2C

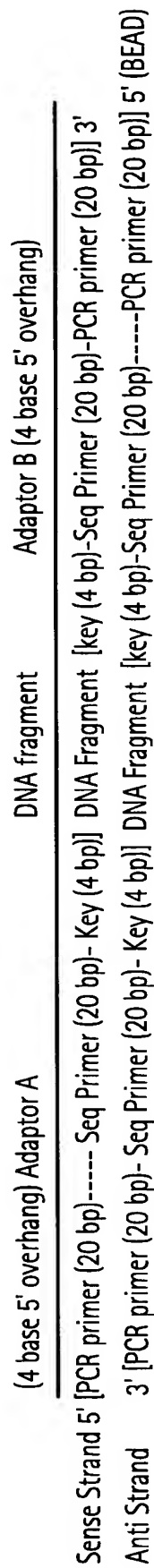


FIG. 3A

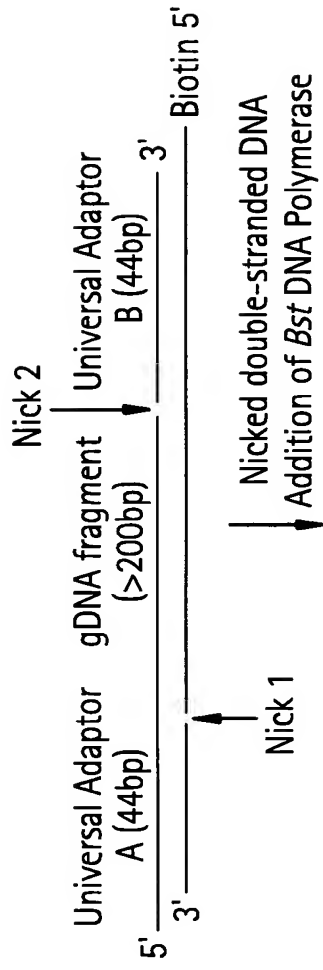


FIG. 3B

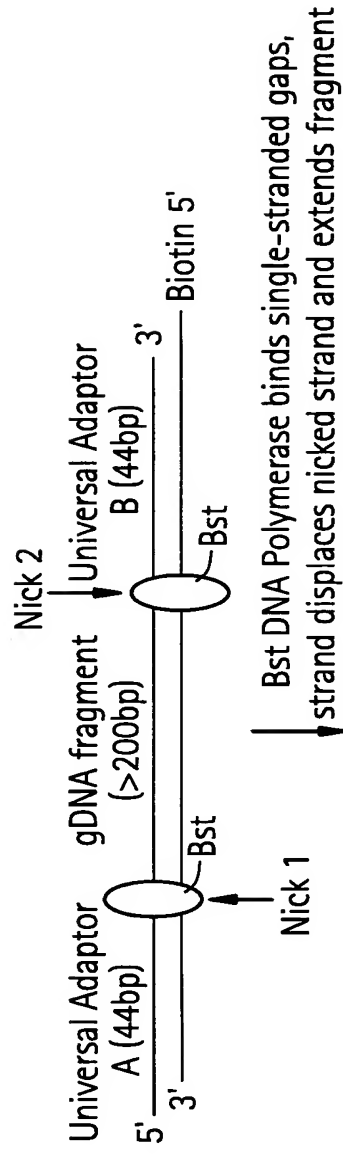


FIG. 3C

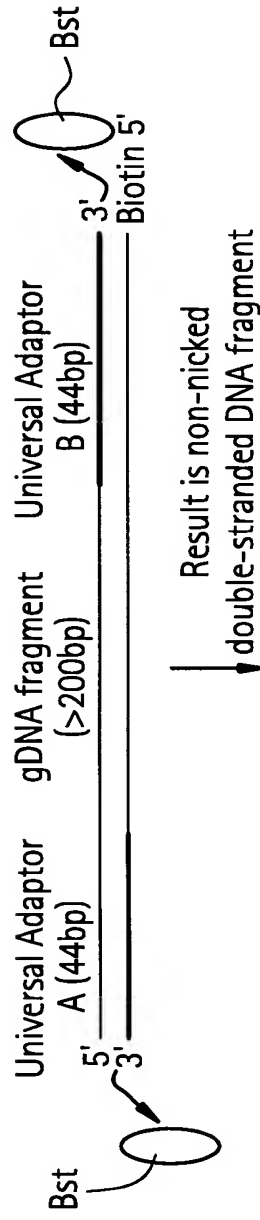


FIG. 3D

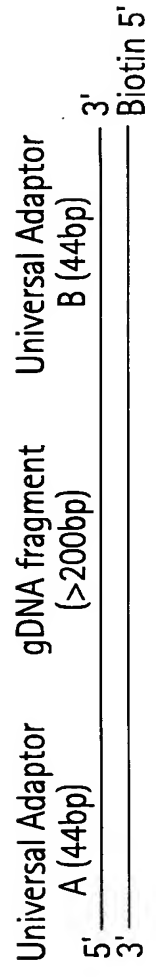
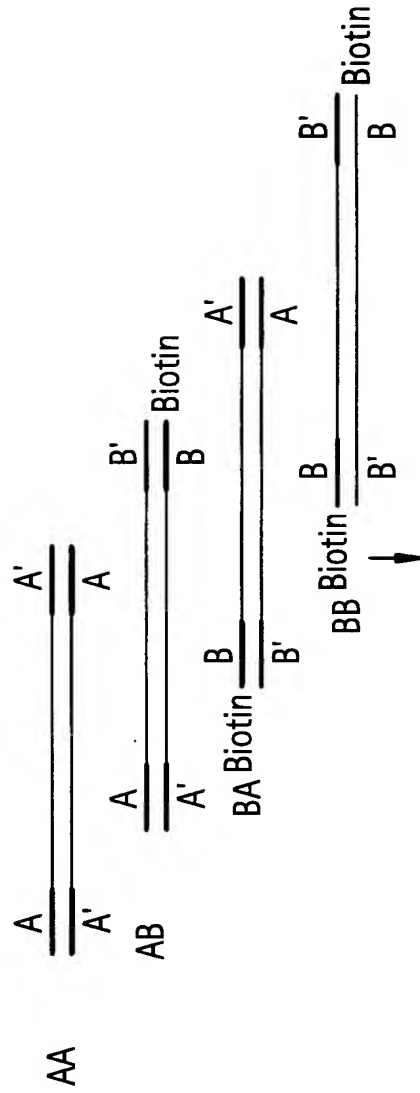


FIG. 4

Possible double-stranded Genomic DNA Library Species:



AB, BA: Single and bound-

ssDNA strands are released  
in the presence of a low salt  
melt solution

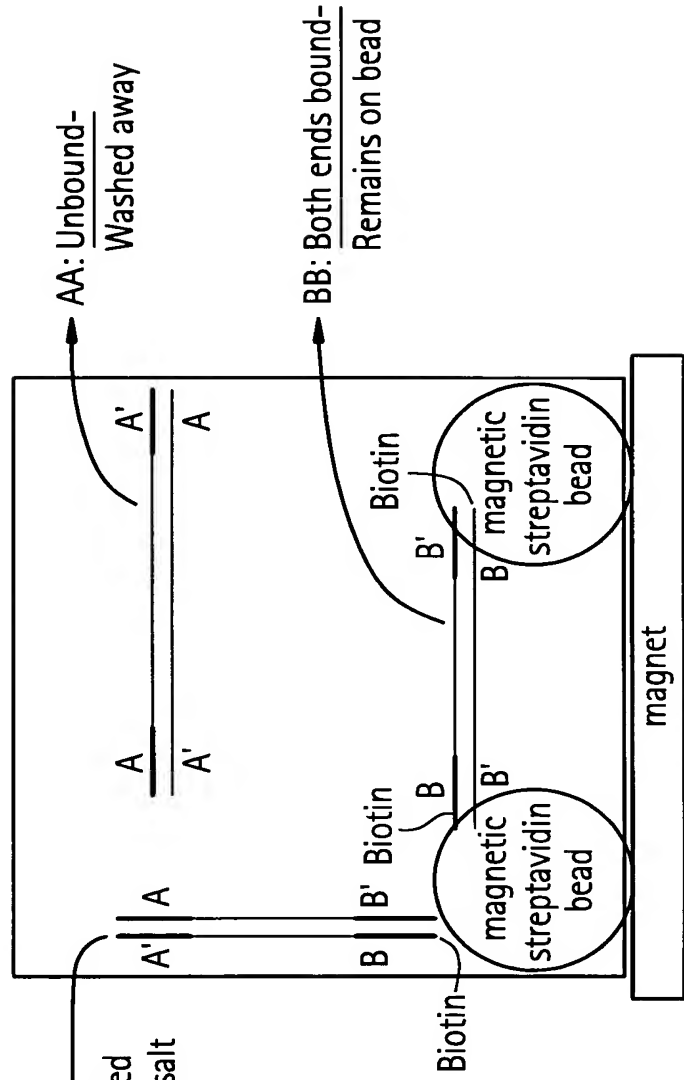


FIG. 5

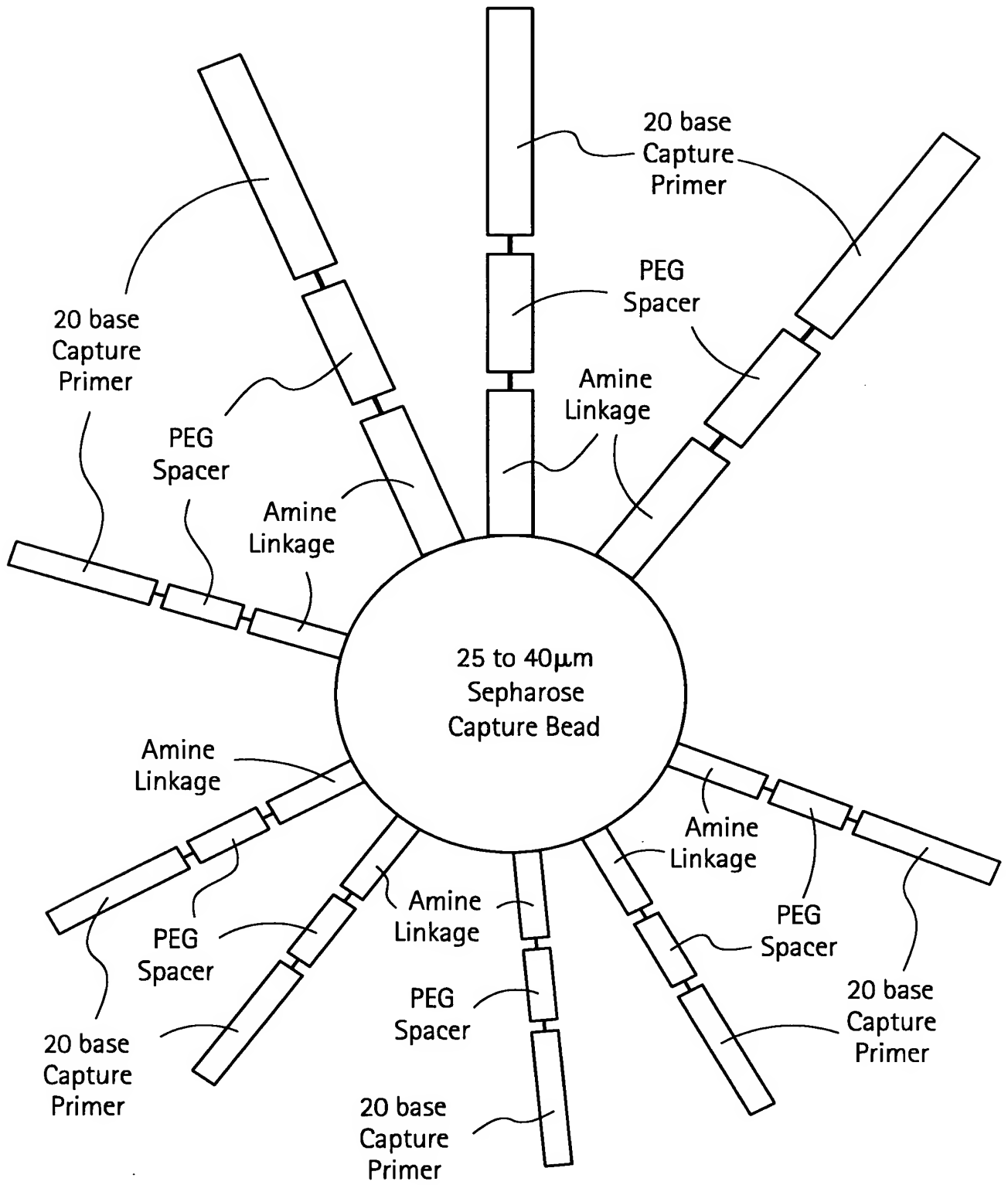


FIG. 6A

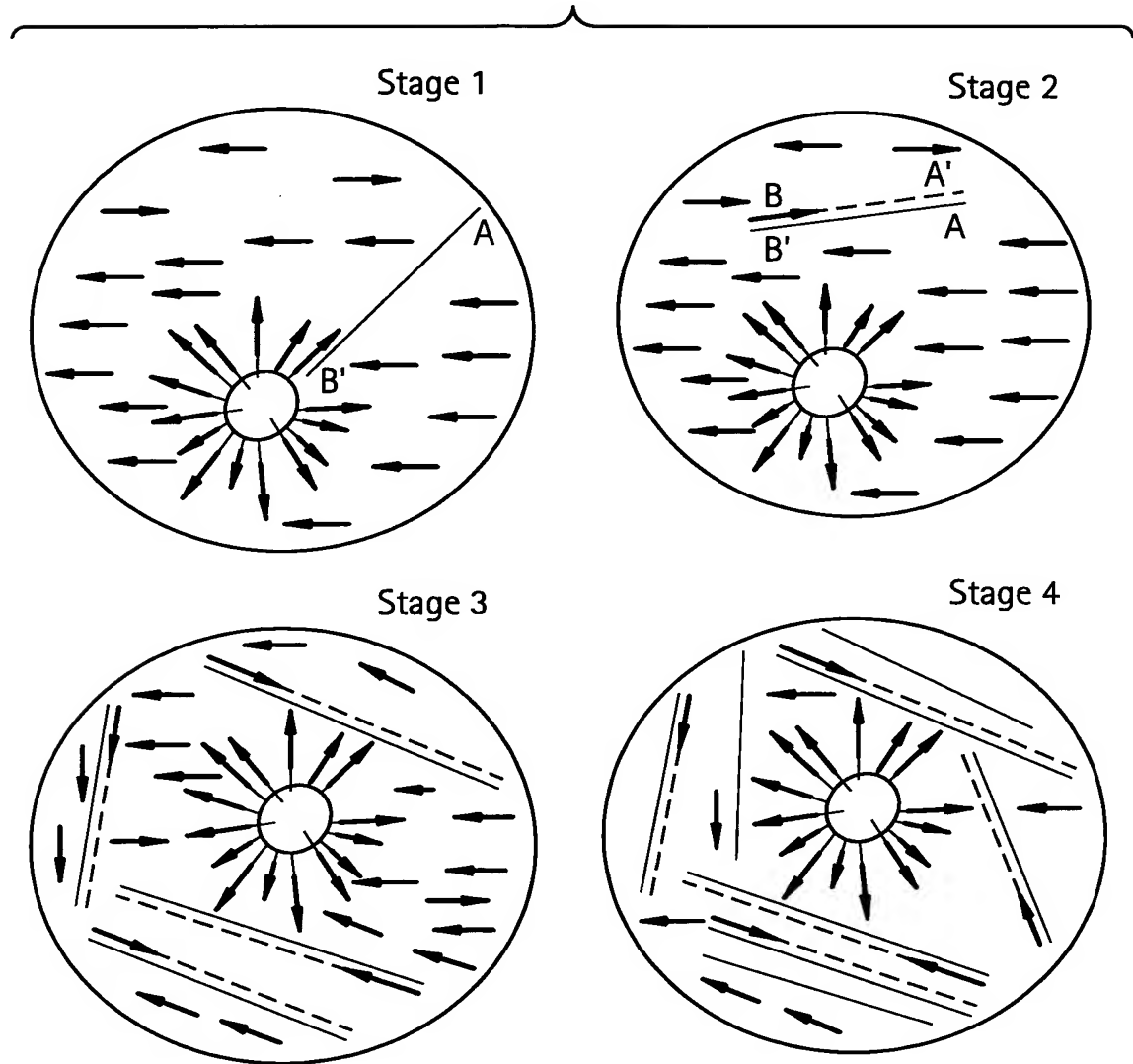




FIG. 6B

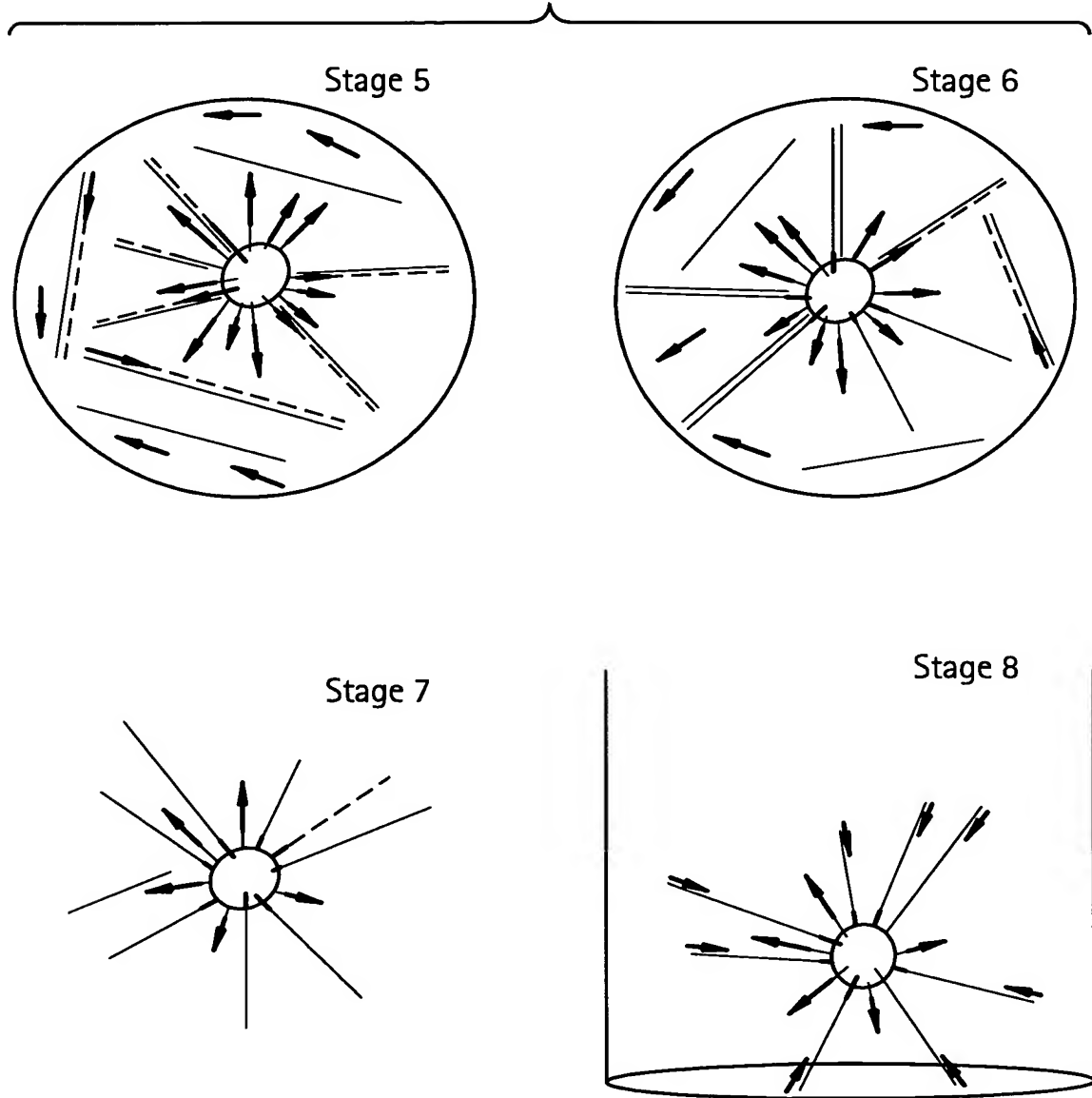


FIG. 7

Schematic Process Flow for Bead Separation

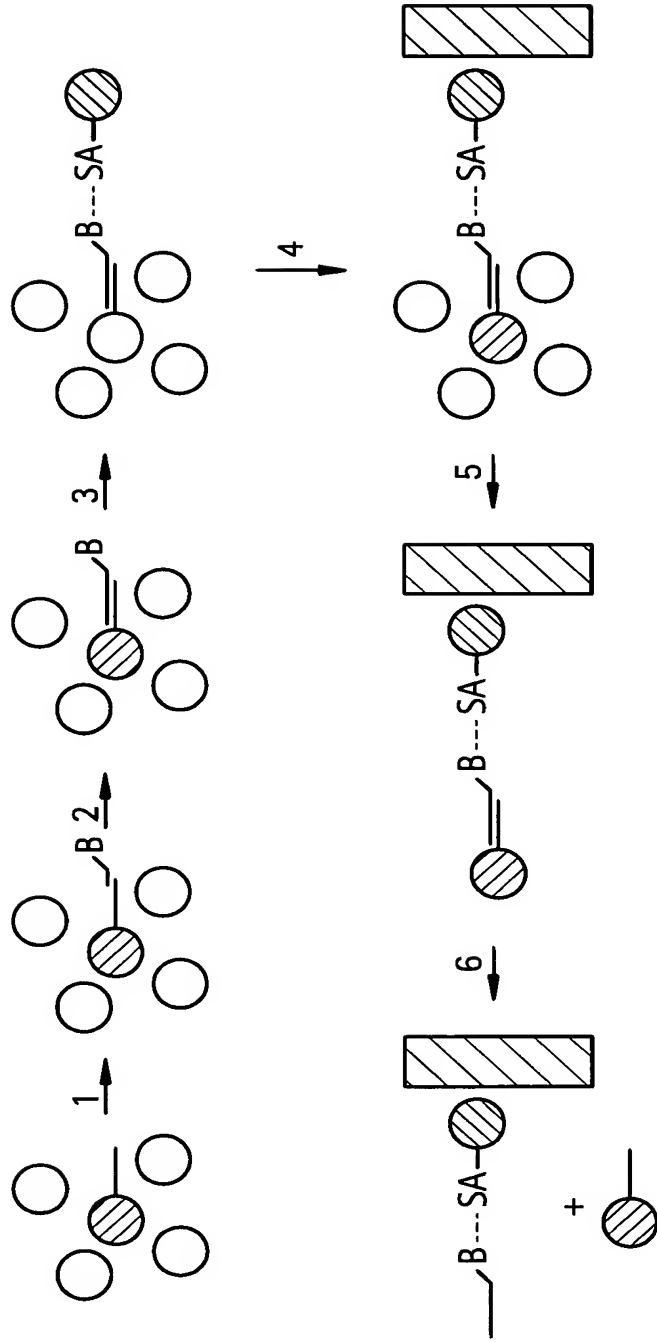


FIG. 8A

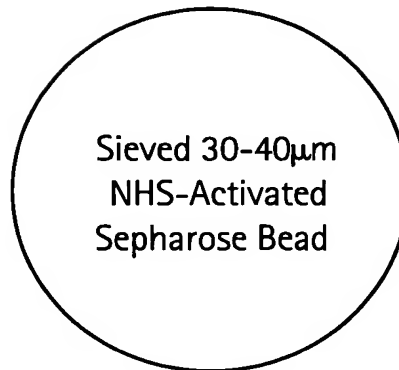


FIG. 8B

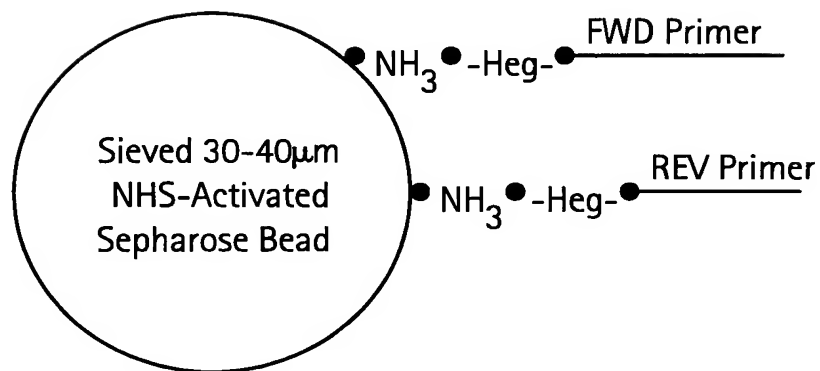


FIG. 8C

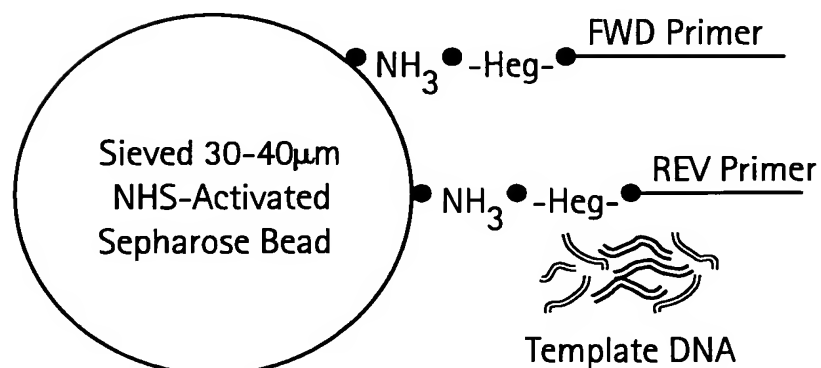


FIG. 8D

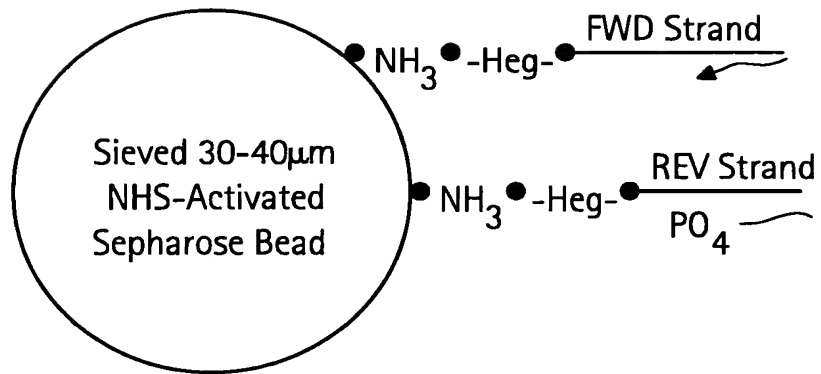


FIG. 8E

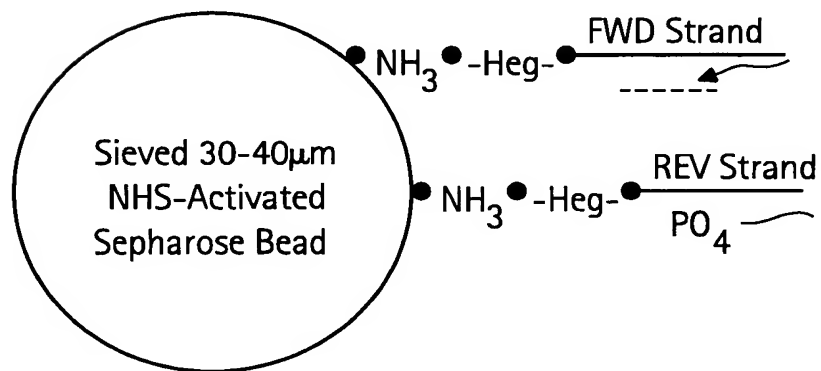


FIG. 8F

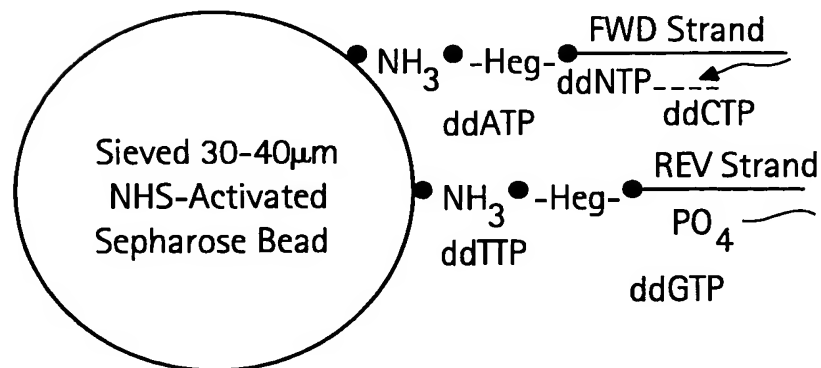


FIG. 8G

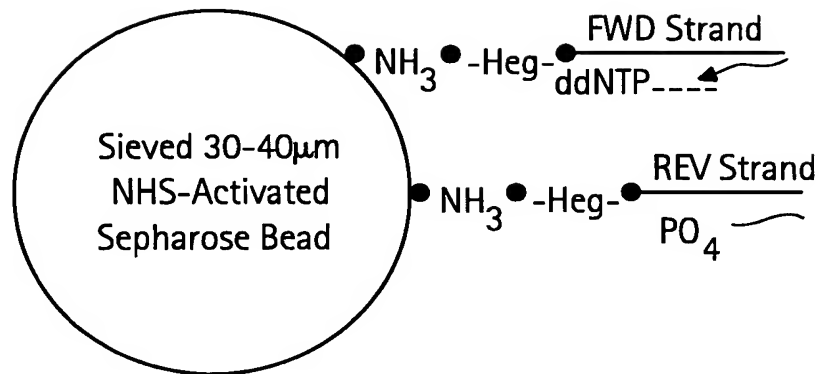


FIG. 8H

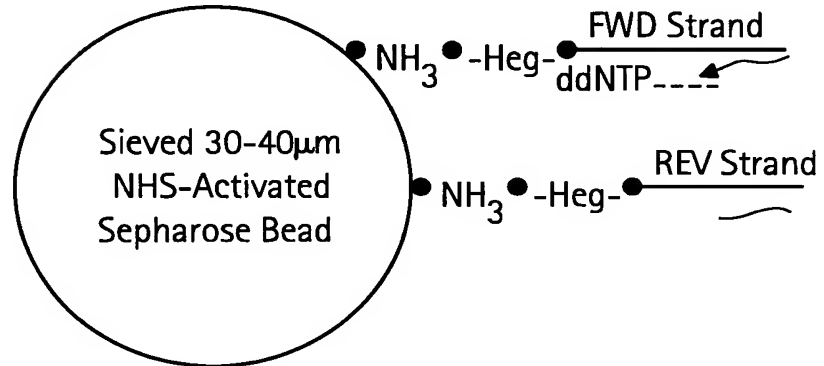


FIG. 8I

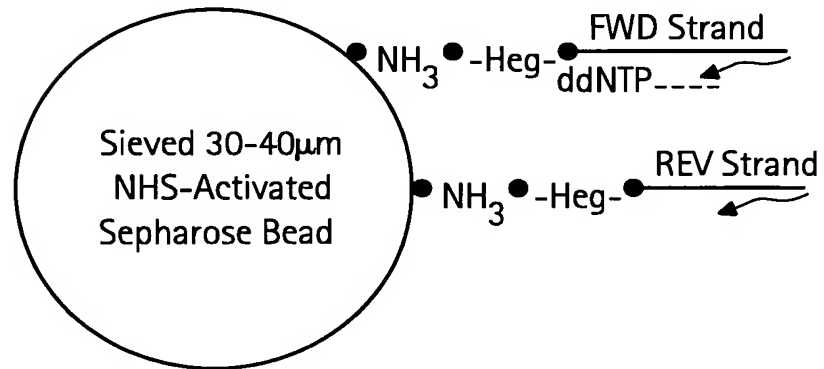


FIG. 8J

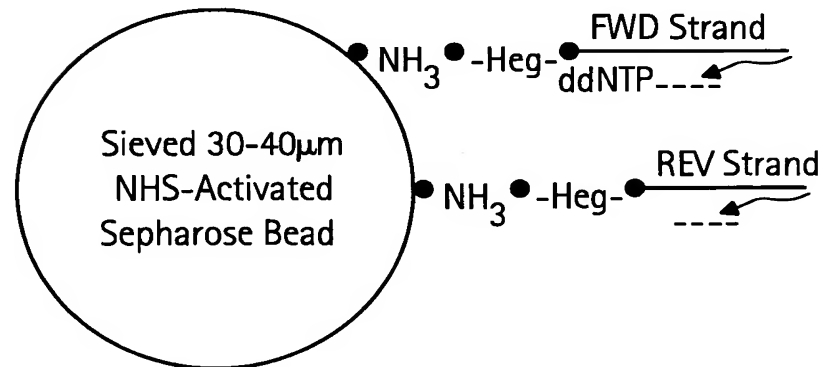


FIG. 9

1\_21\_03 N7 from 1\_14\_03 10X Double Strand

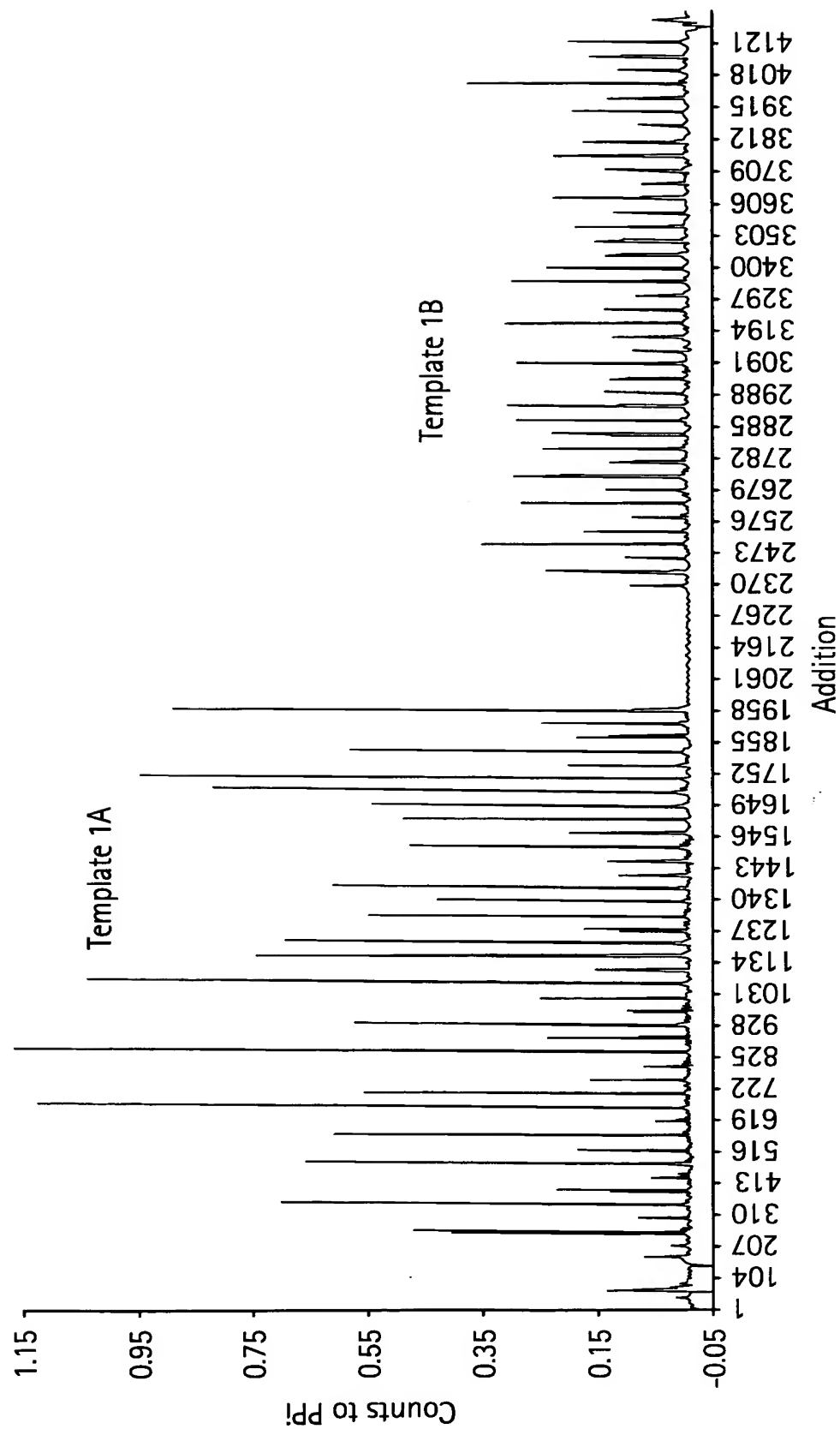


FIG. 10A

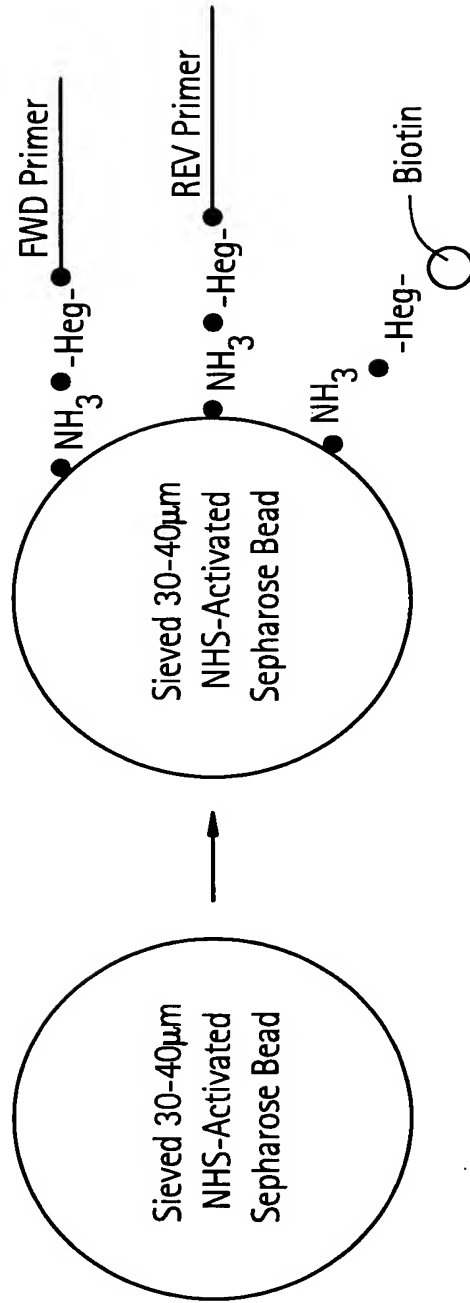


FIG. 10B

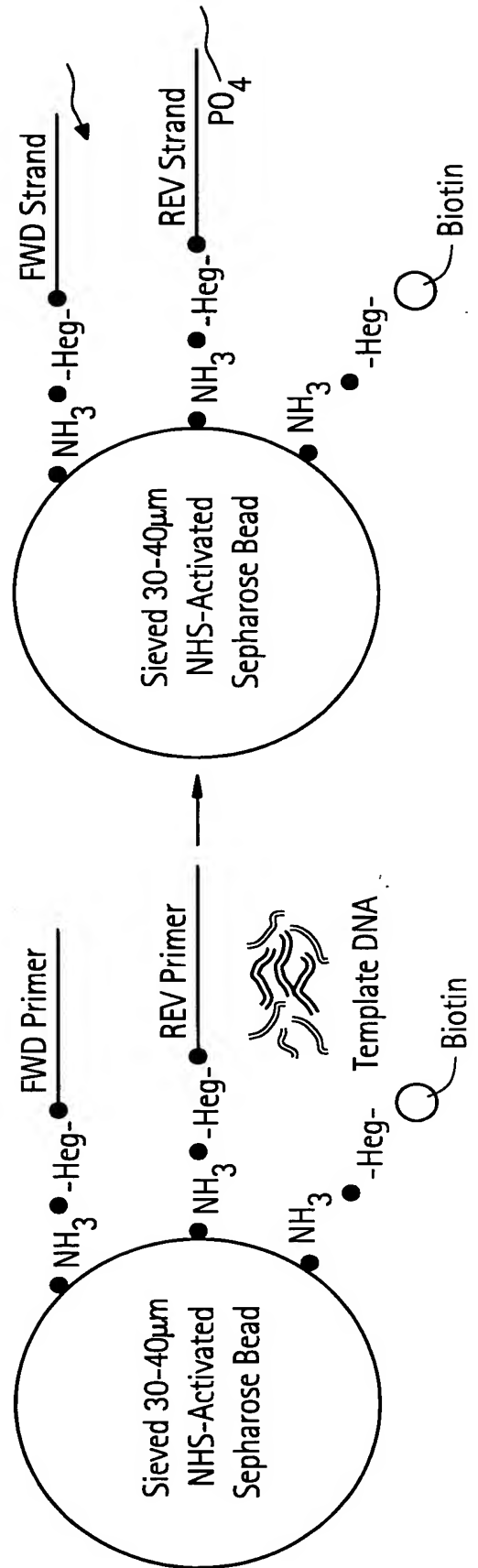


FIG. 10C

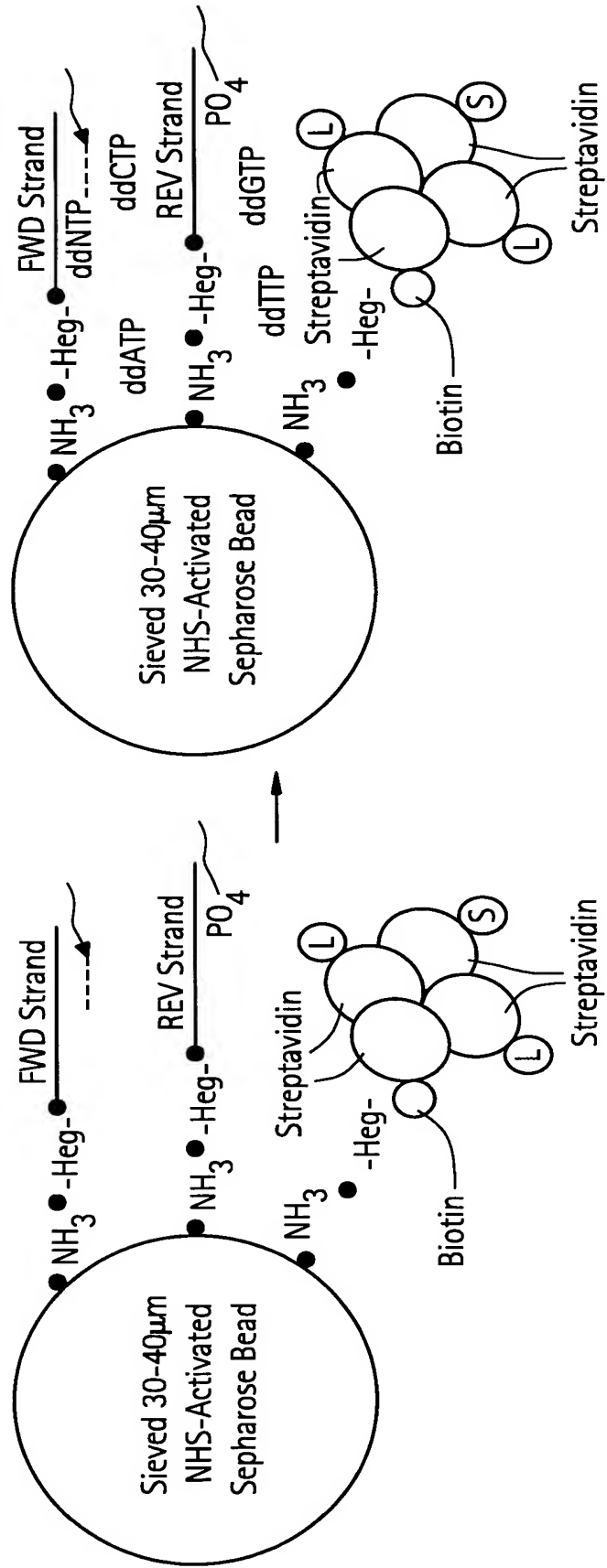




FIG. 10D

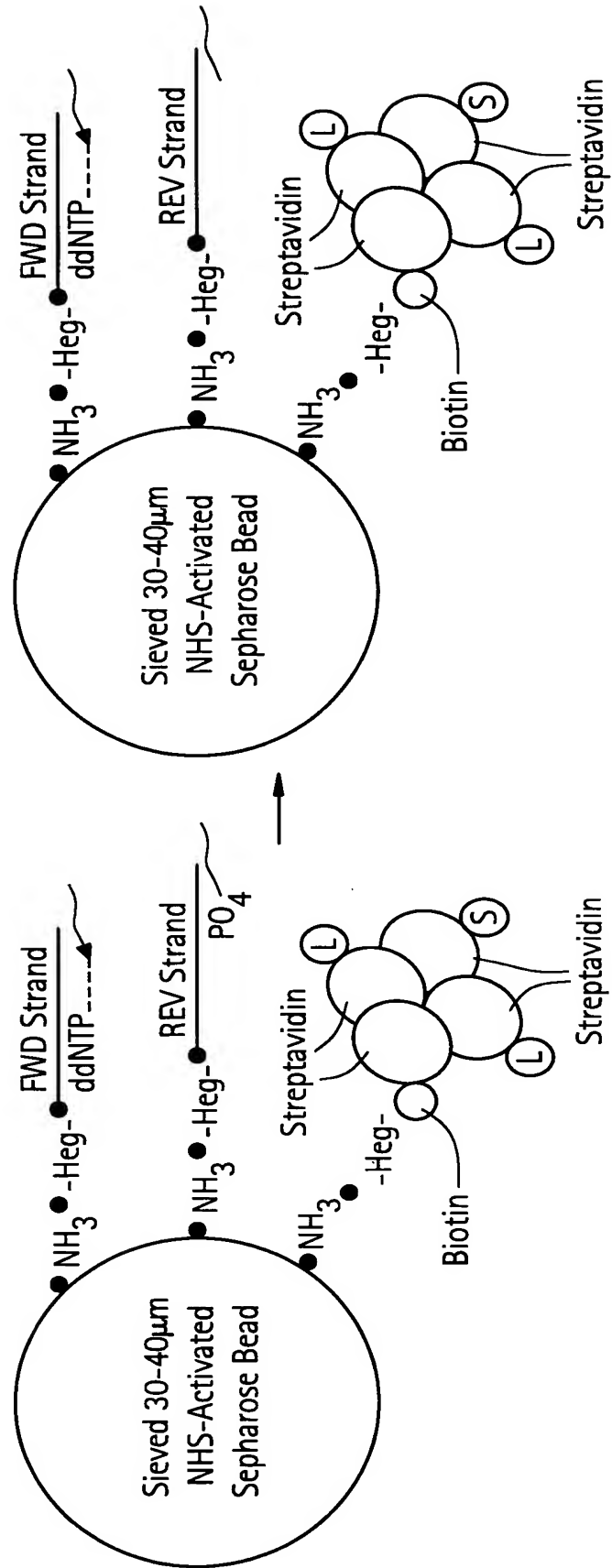


FIG. 10E

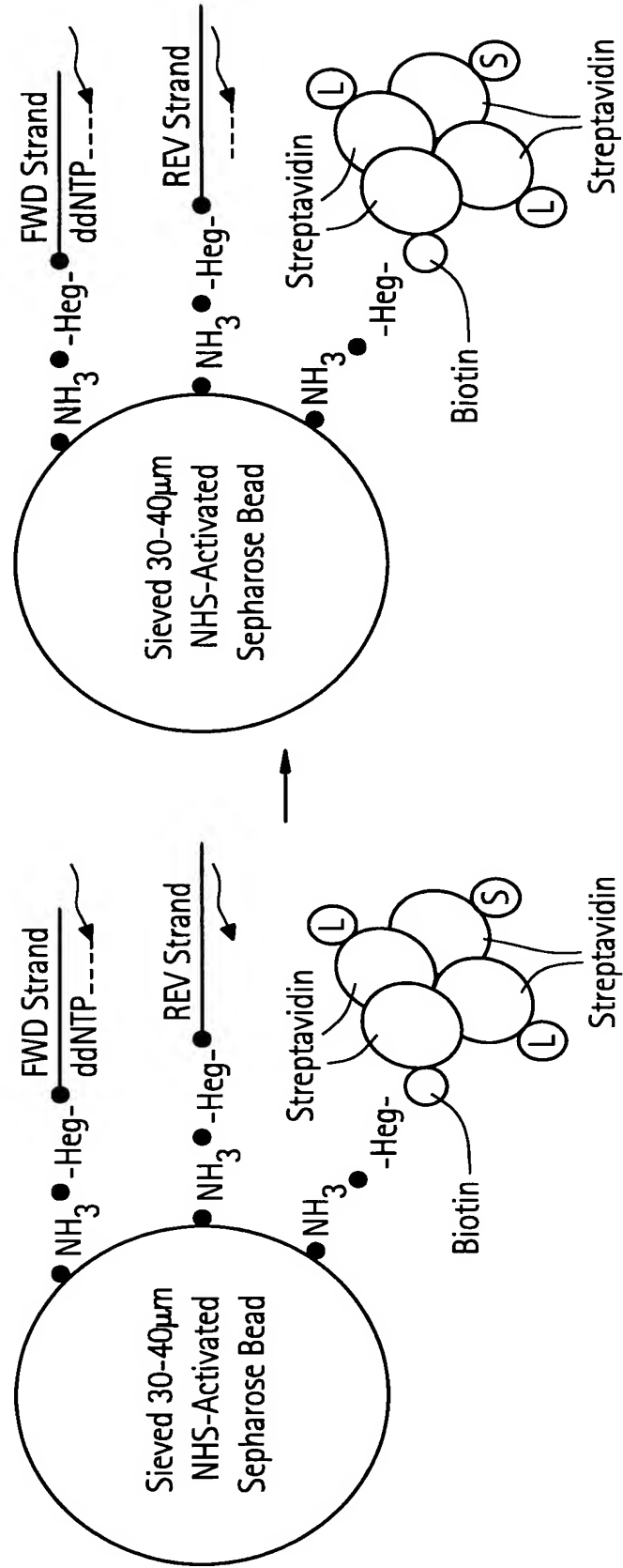
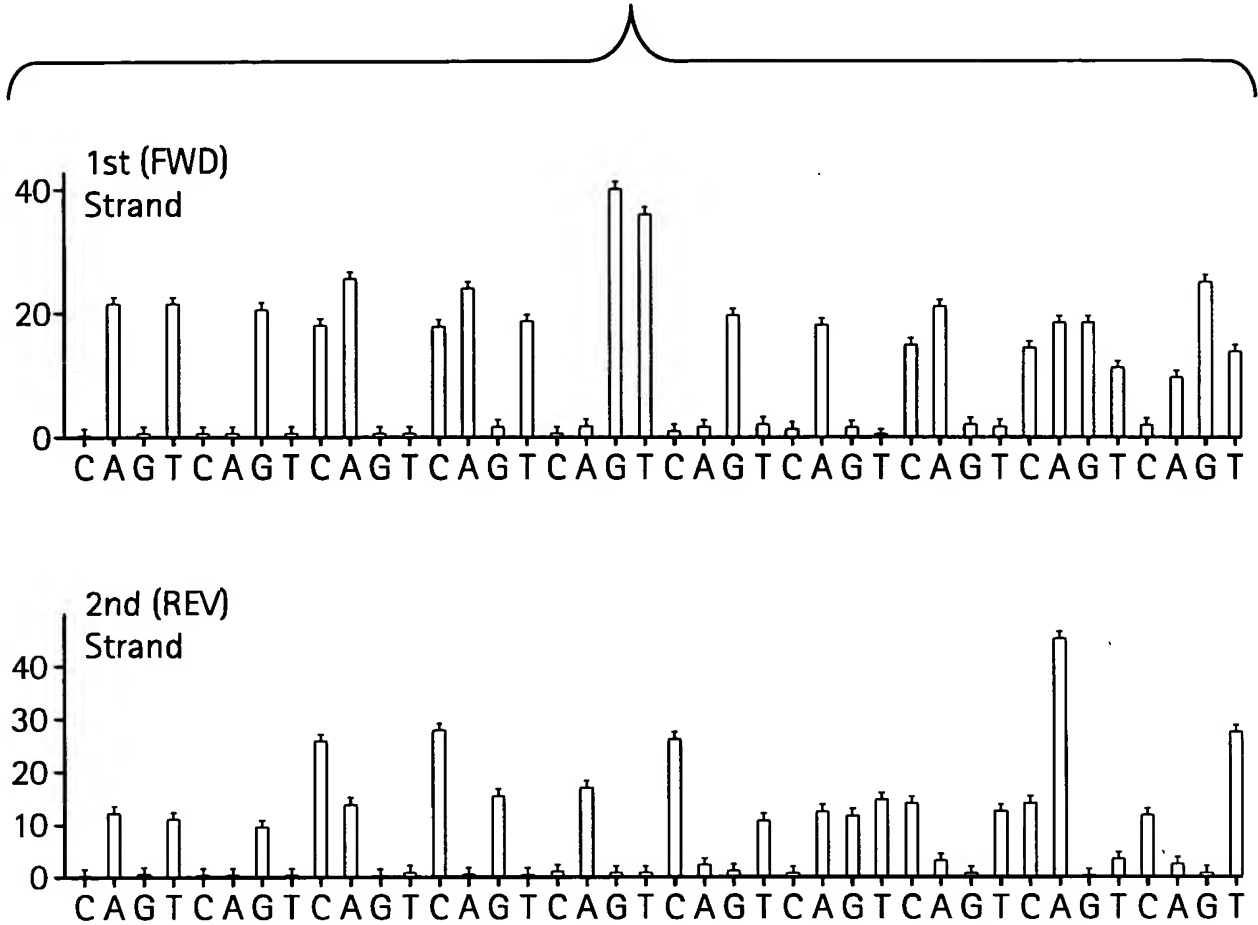


FIG. 10F



1st Strand  
(FWD)

| Sample  | Well Location        | Sequence                | Perfect Match Length |
|---------|----------------------|-------------------------|----------------------|
| F6_14_1 | 00001_1362_1660.well | ATGCACATGGTTGACACAGTGGT | 22                   |

ATGC ACATGGTTGACACAGTGG

2nd Strand  
(REV)

| Sample  | Well Location        | Sequence                  | Perfect Match Length |
|---------|----------------------|---------------------------|----------------------|
| F6_14_1 | 00003_1363_1660.well | ATGCCACCGACCTAGTCTCAAACCT | 25                   |

ATGC CACCGACCTAGTCTCAAACCT

FIG. 11A

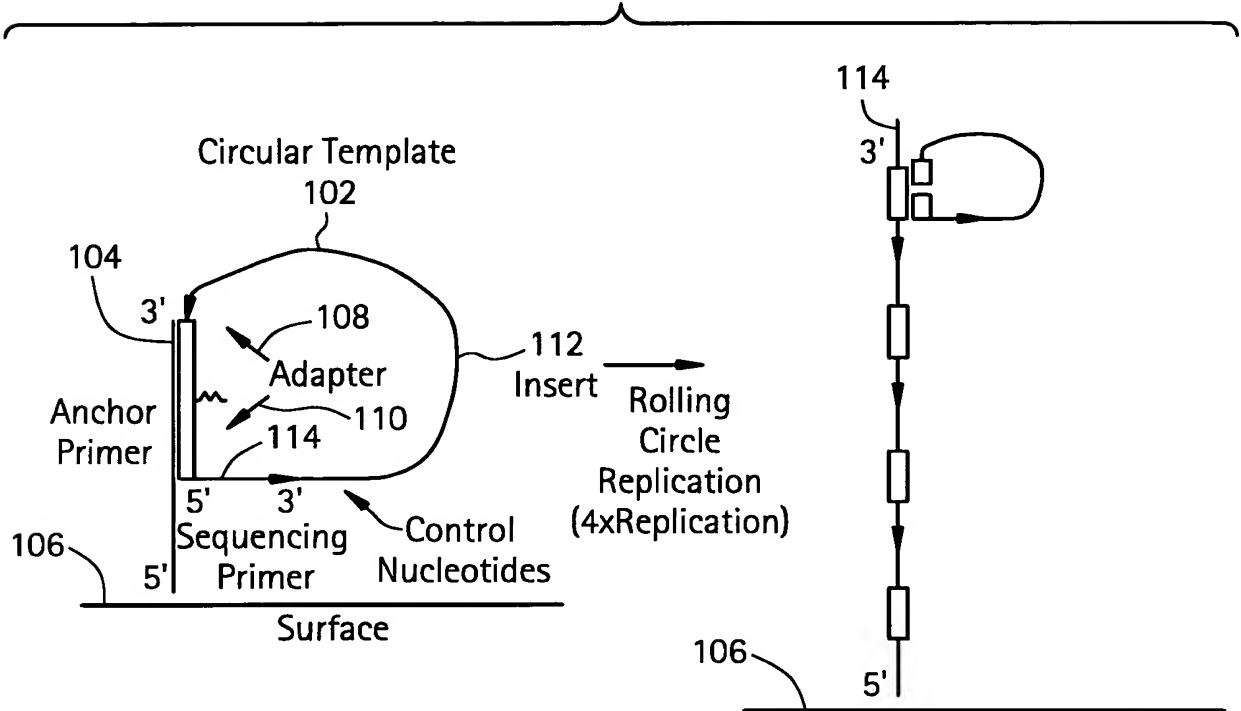


FIG. 11B

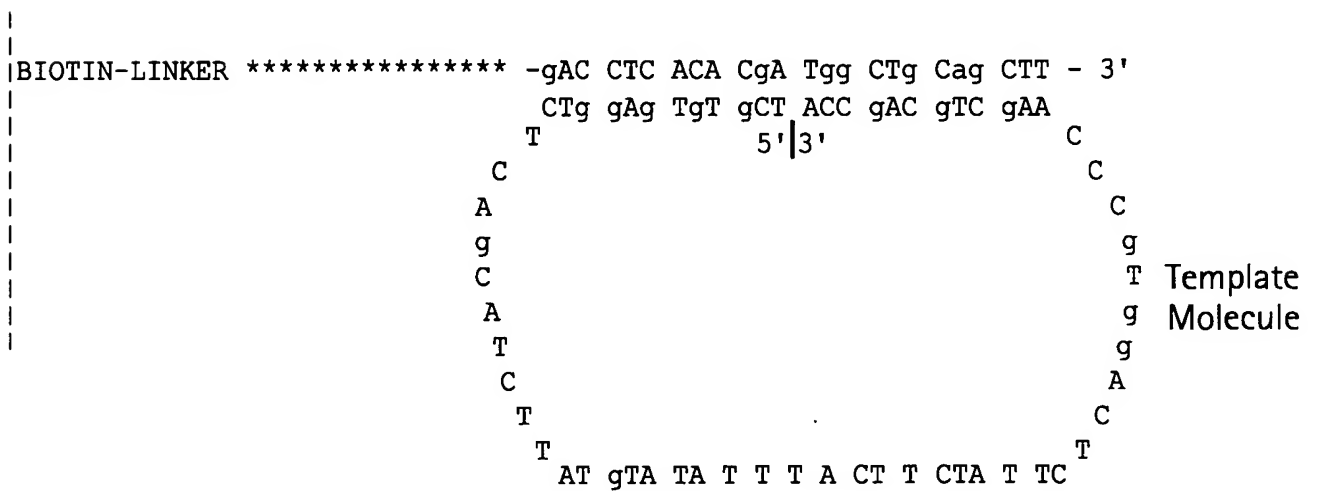


FIG. 11C

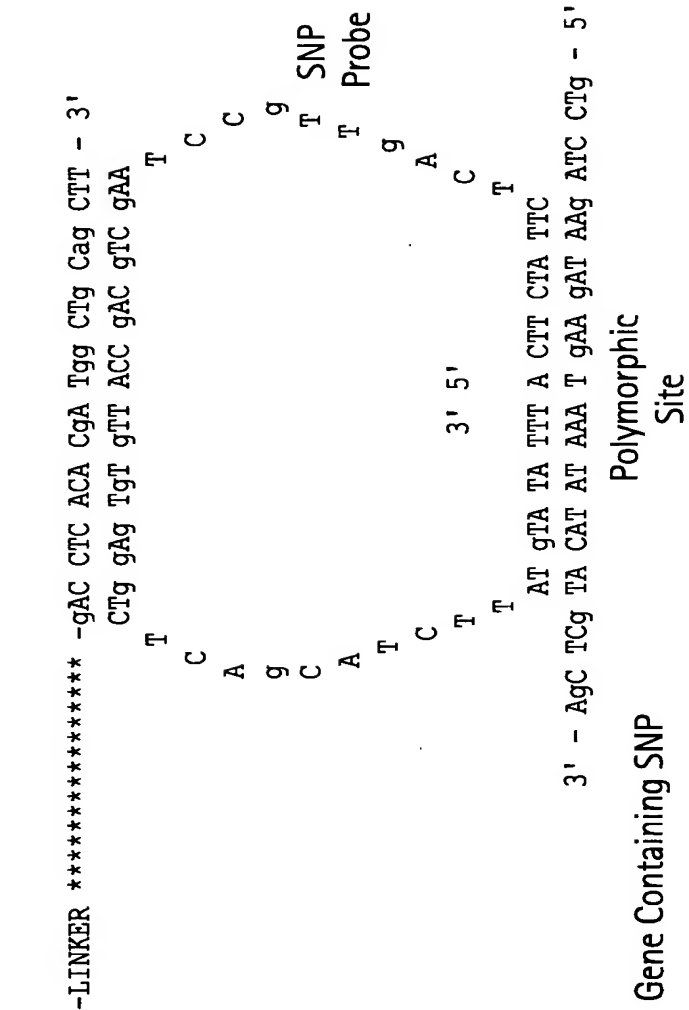


FIG. 11D

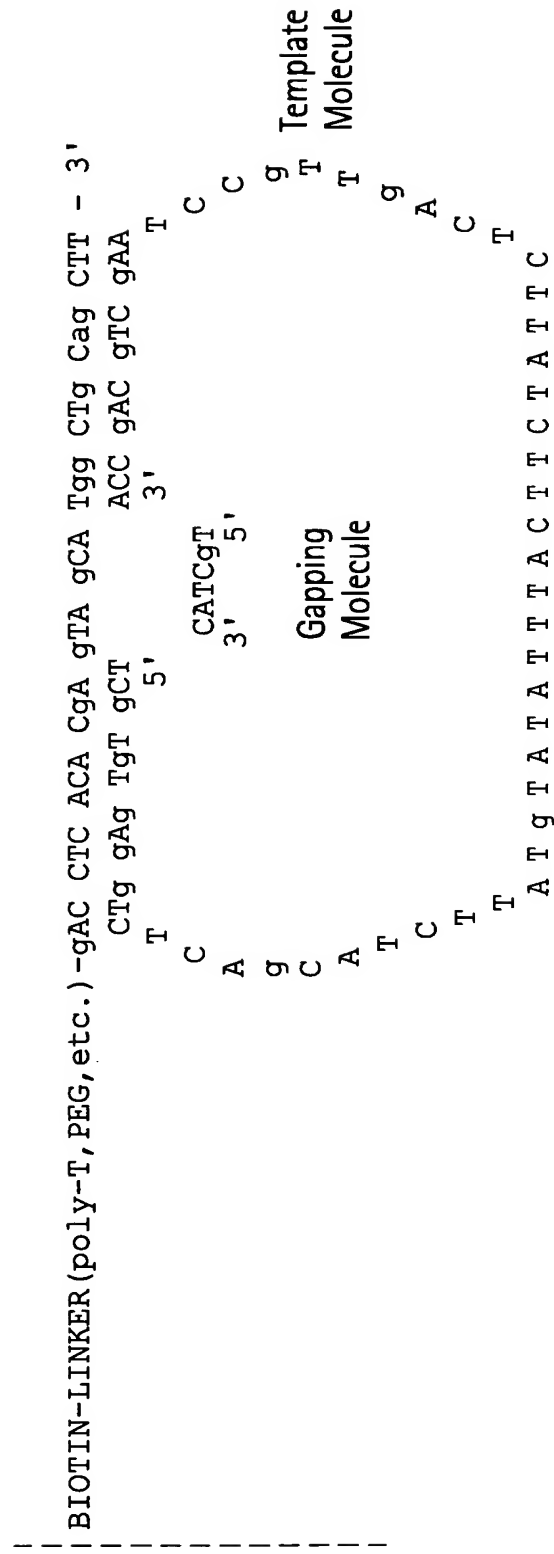


FIG. 12

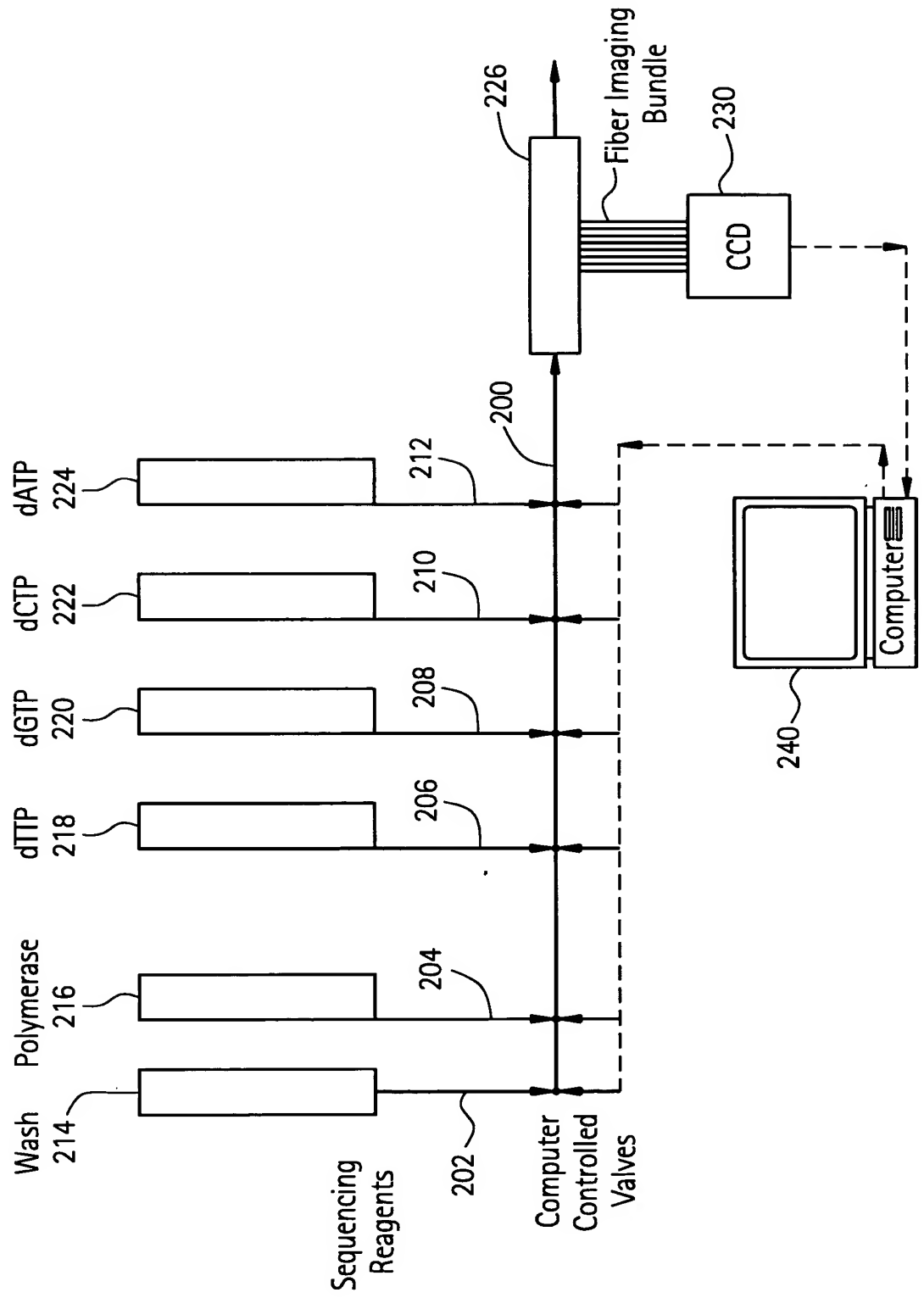


FIG. 13

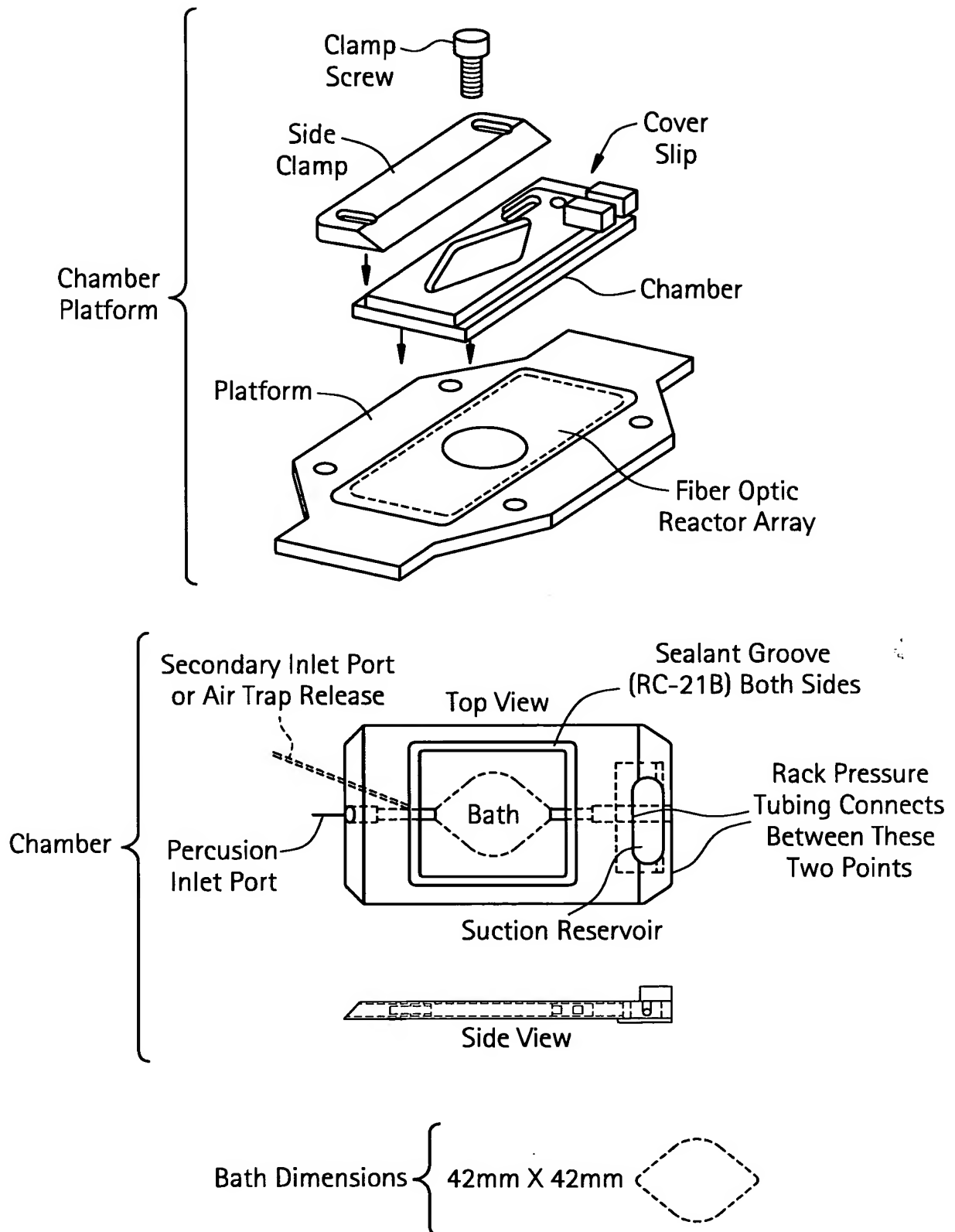




FIG. 14

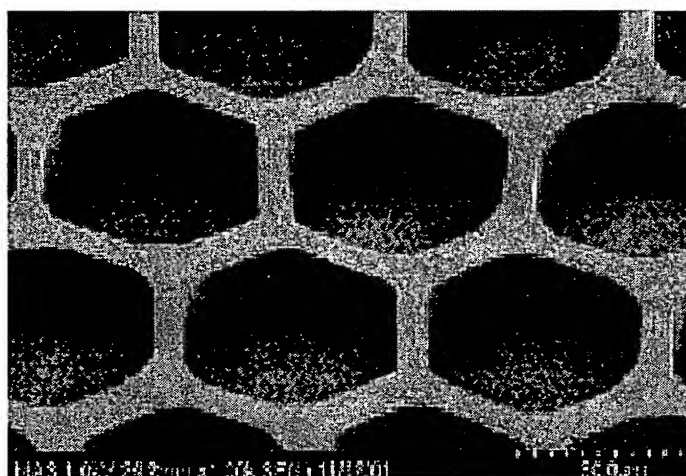
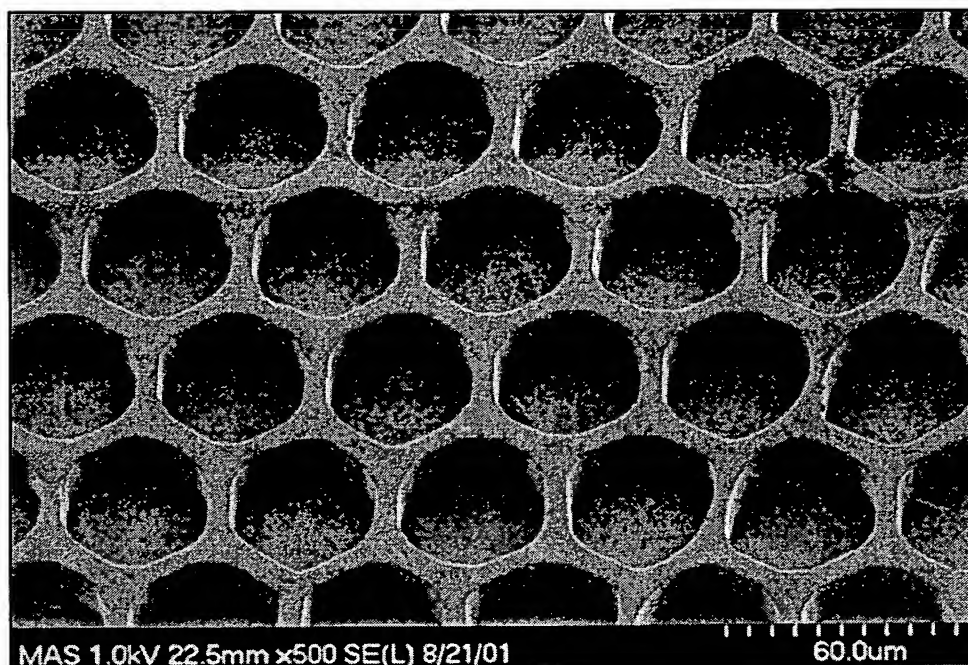


FIG. 15

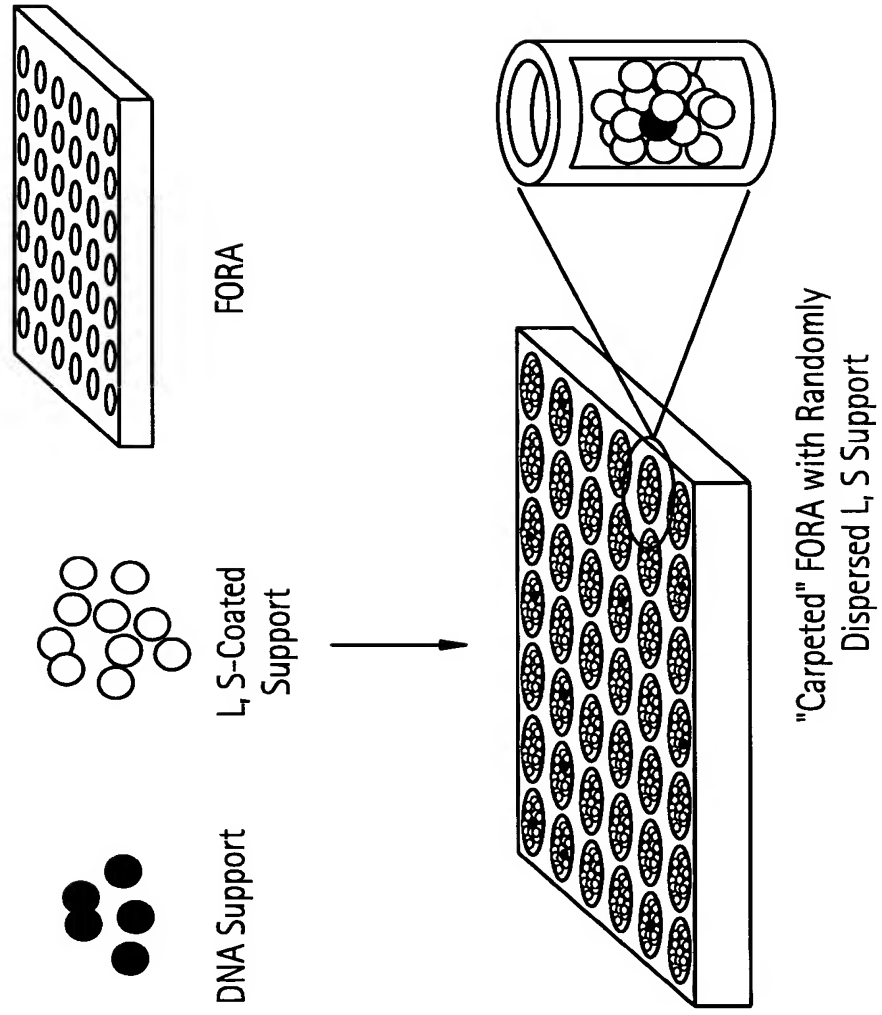


FIG. 16

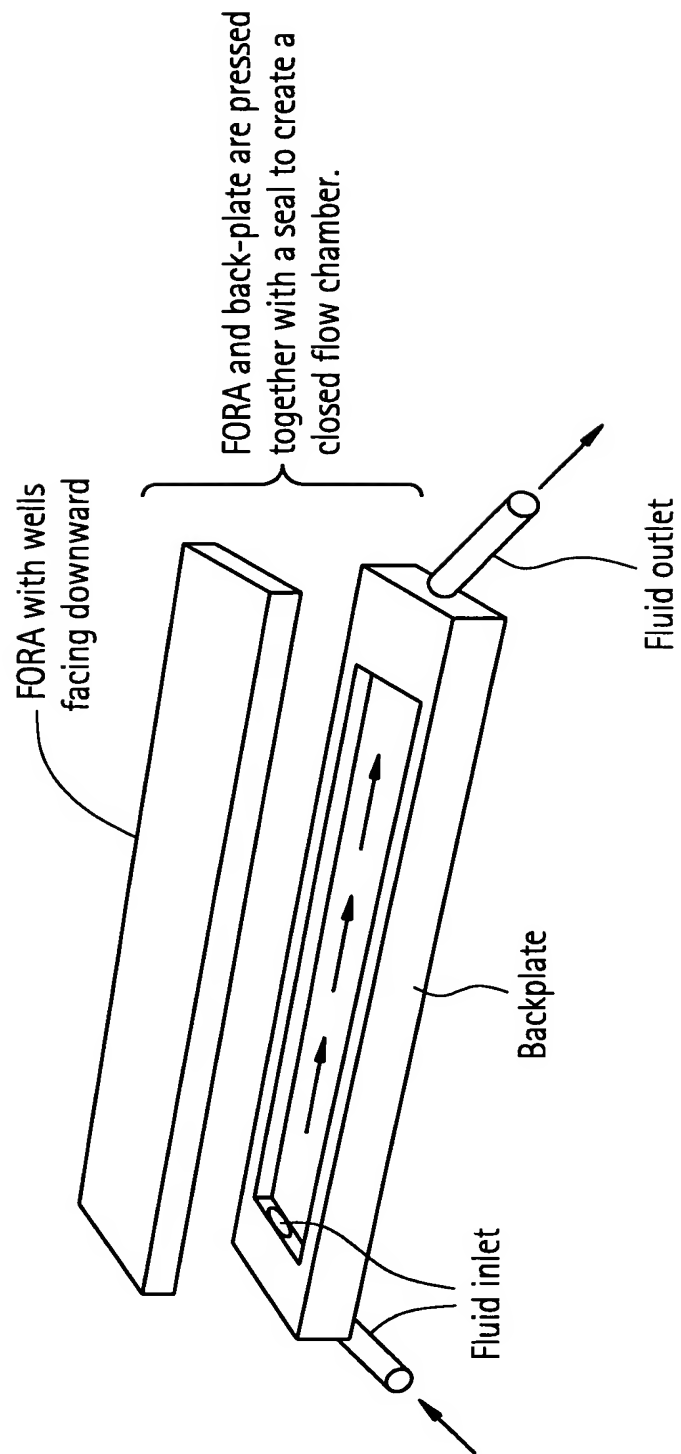


FIG. 17

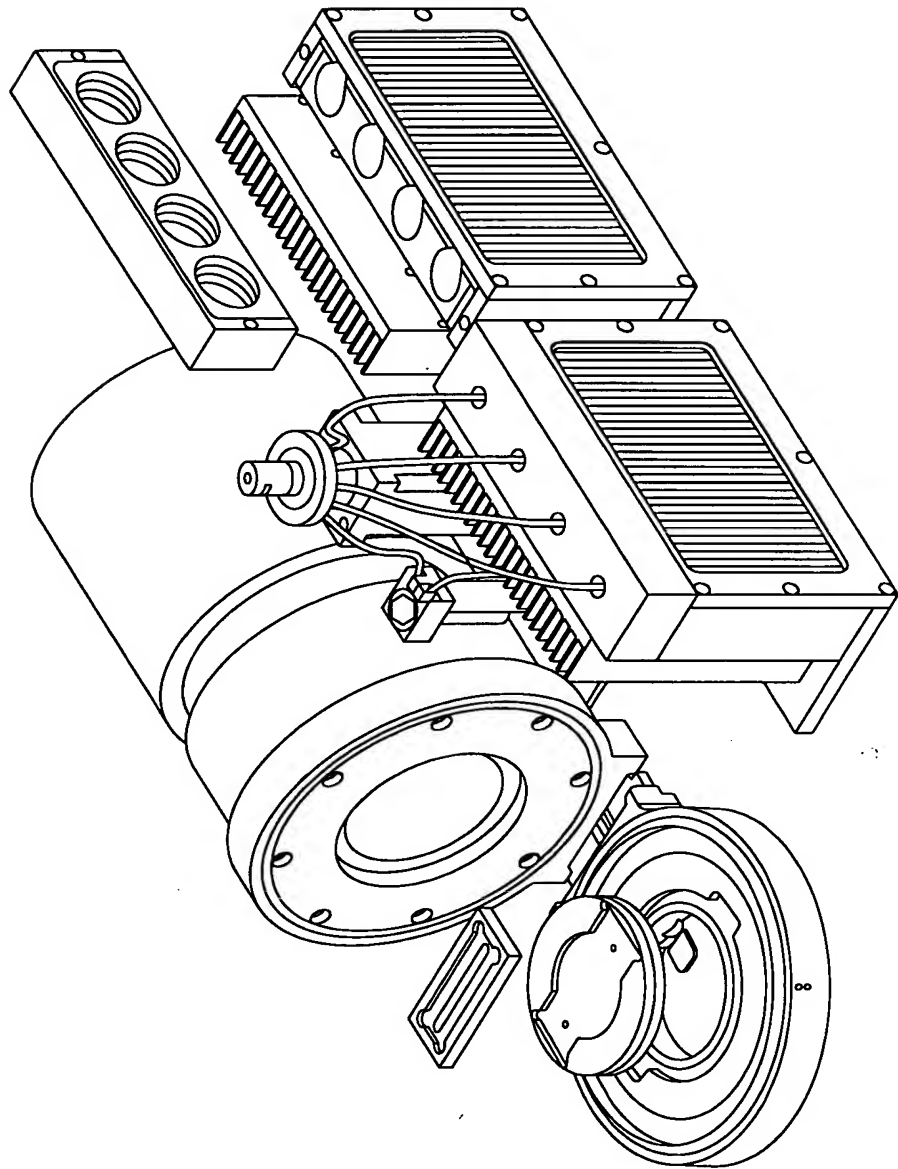


FIG. 18

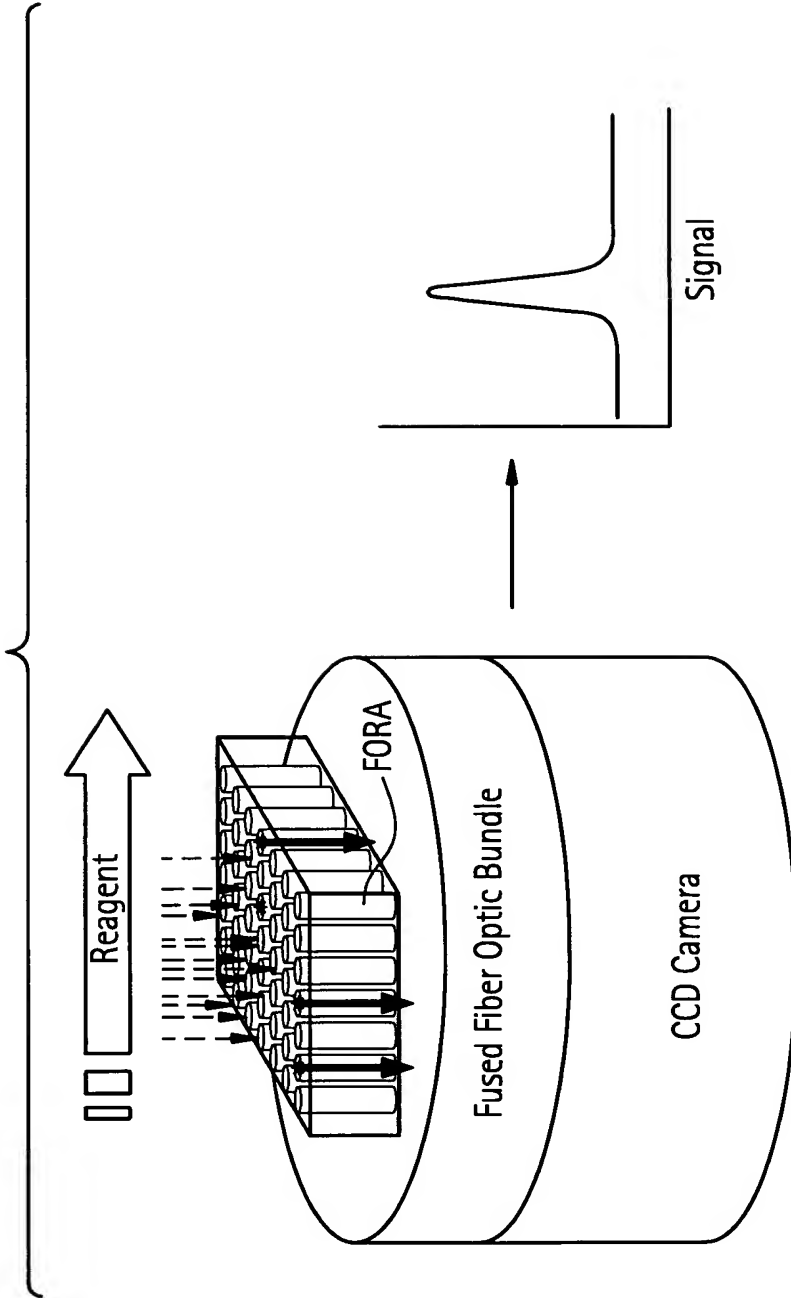


FIG. 19

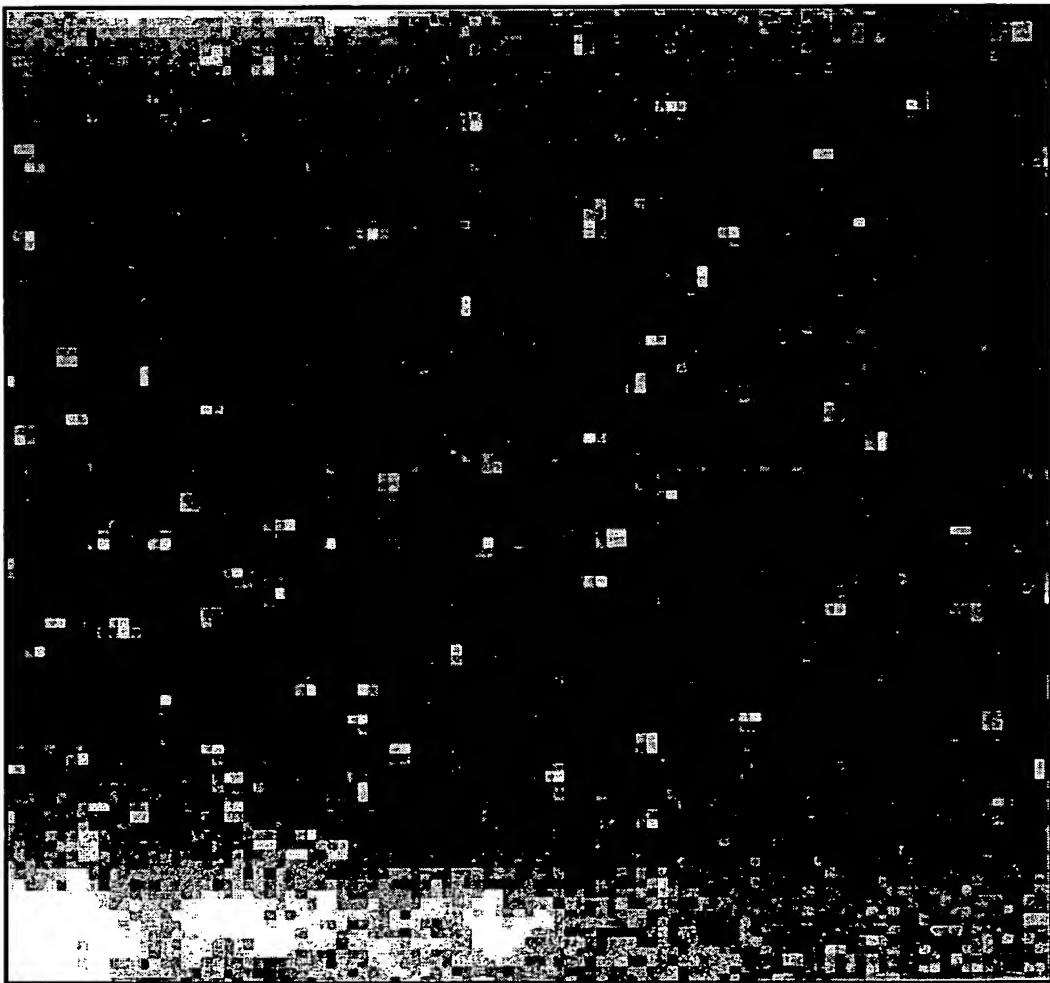


FIG. 20

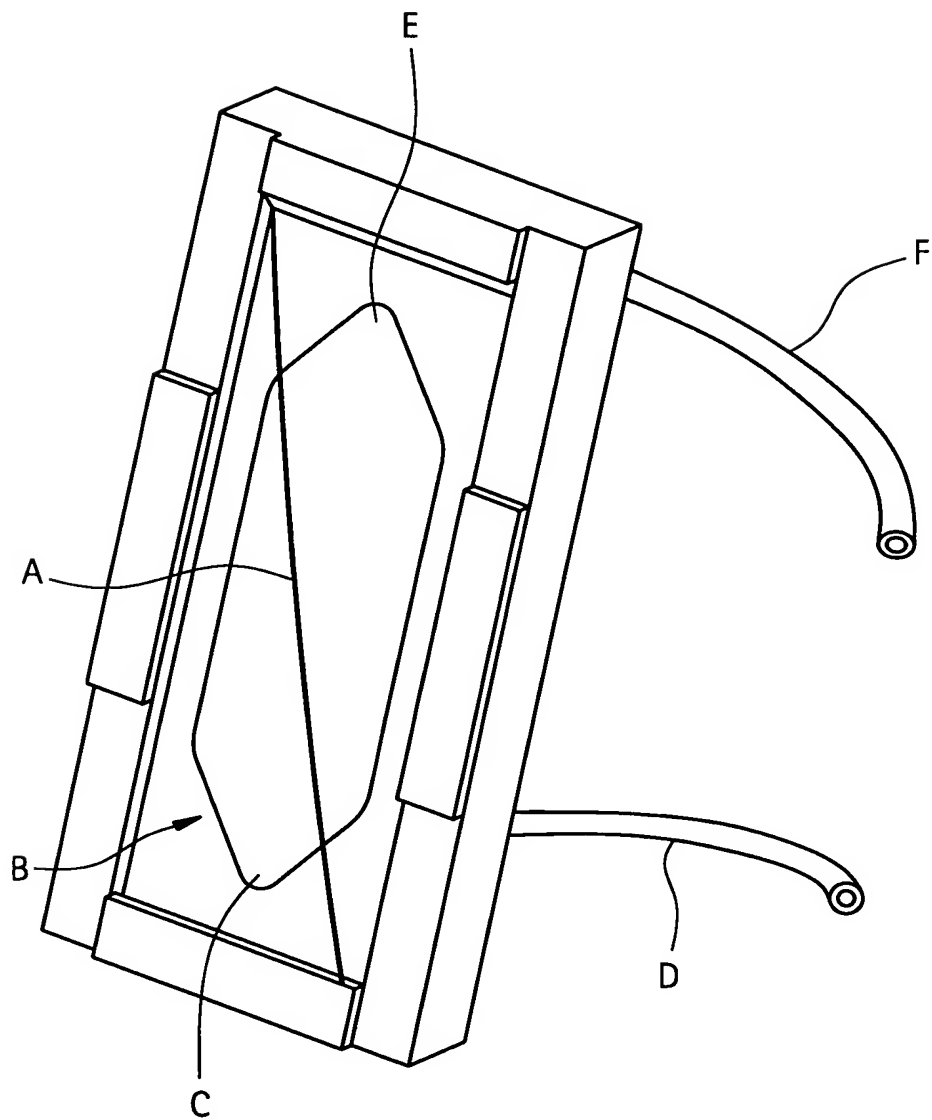


FIG. 21

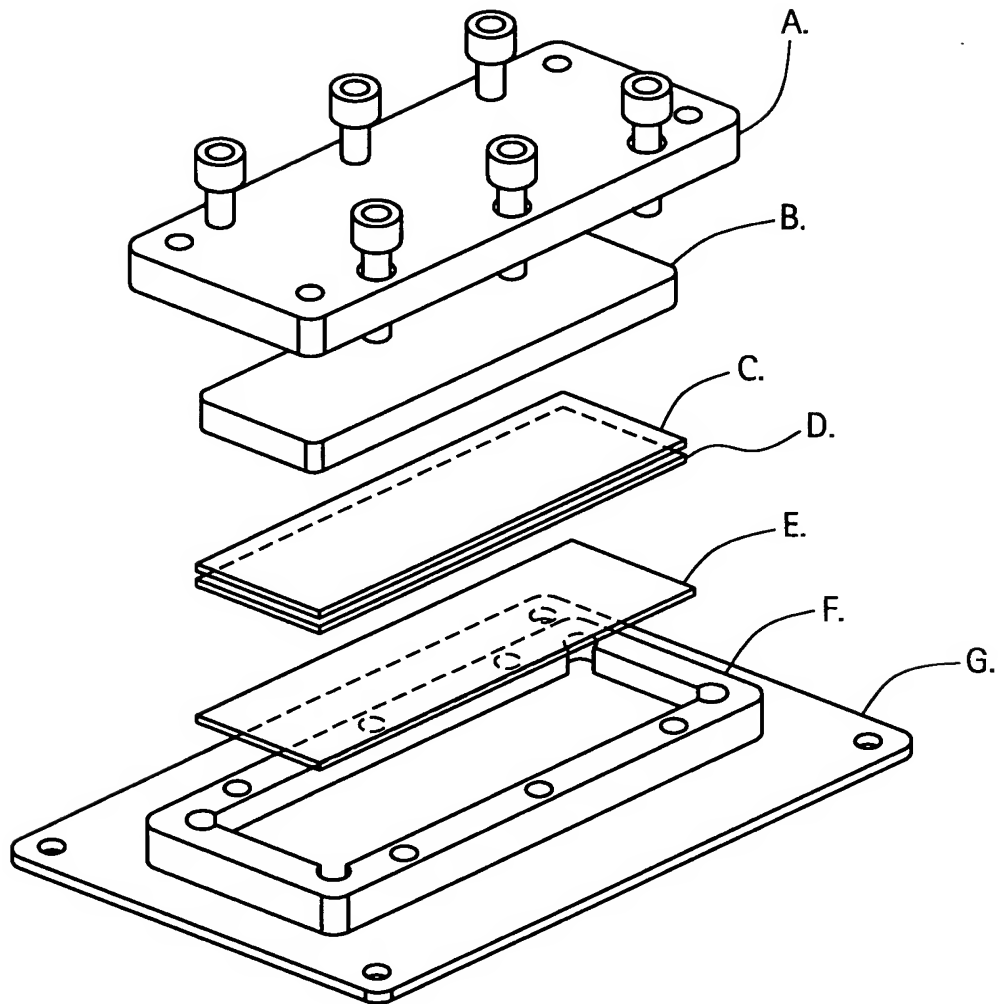




FIG. 22

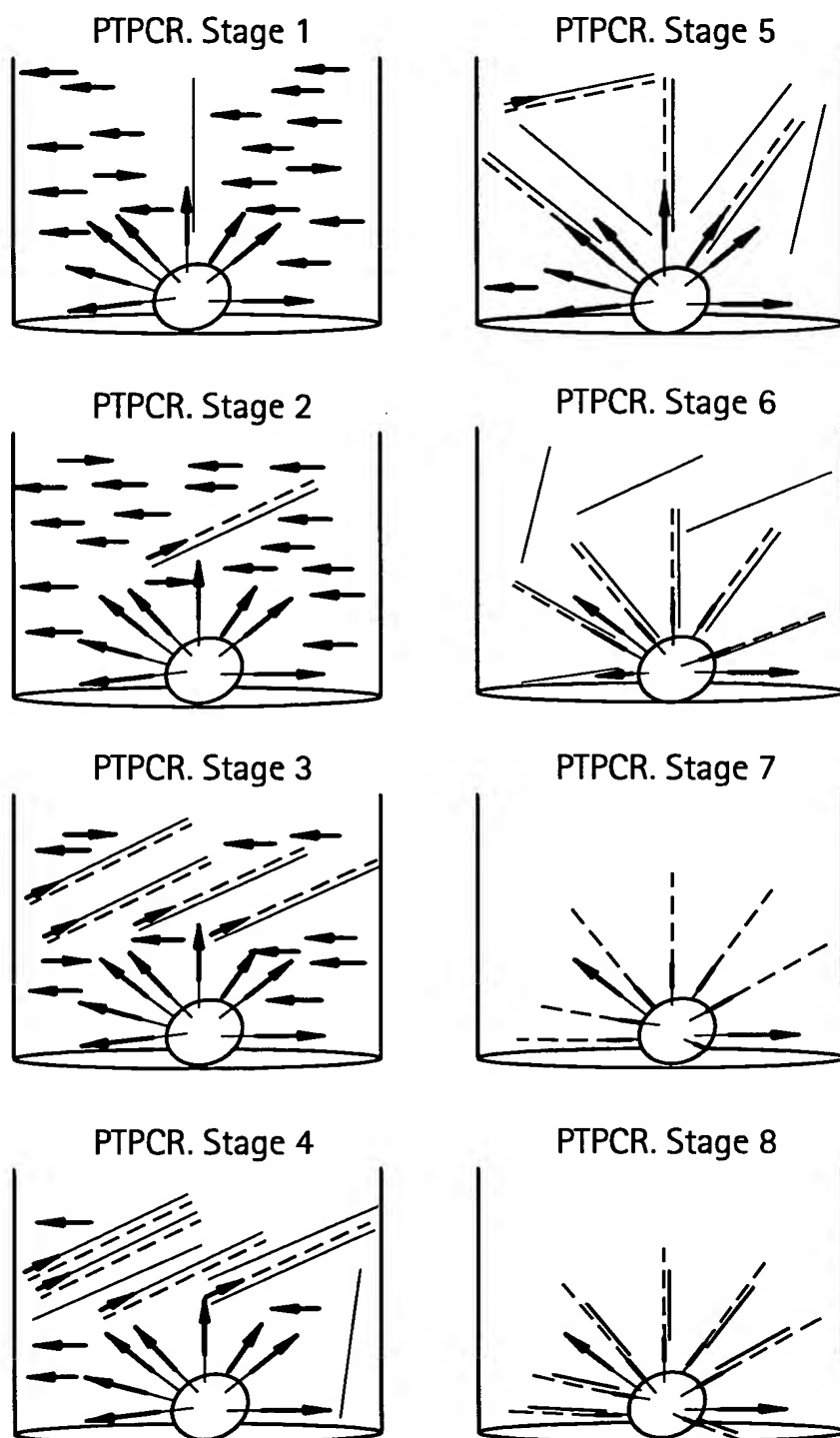


FIG. 23A

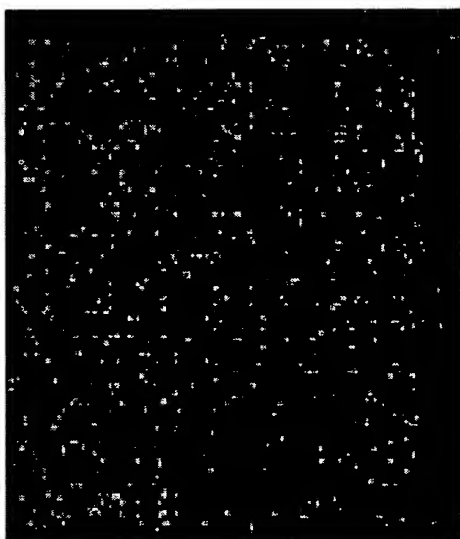


FIG. 23B



FIG. 23C



FIG. 24

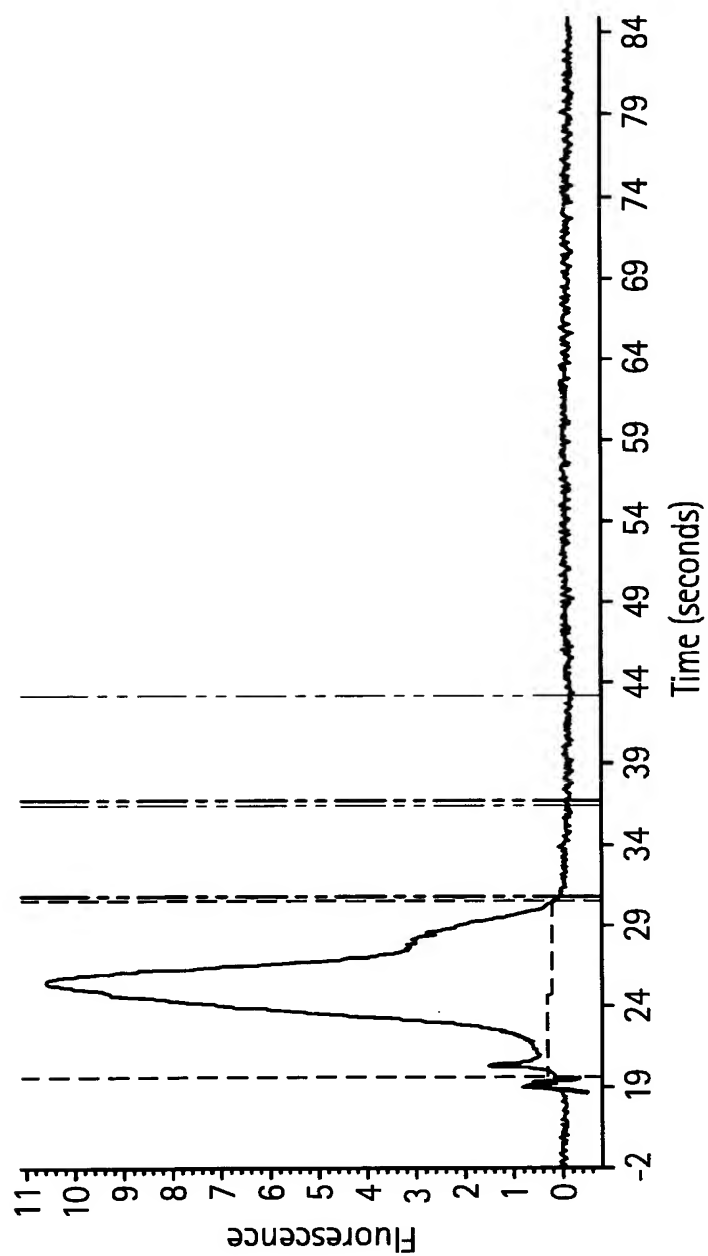


FIG. 25

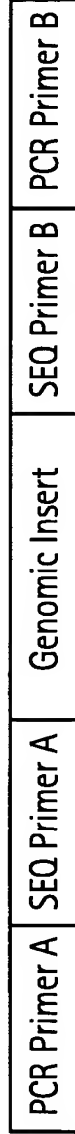


FIG. 26

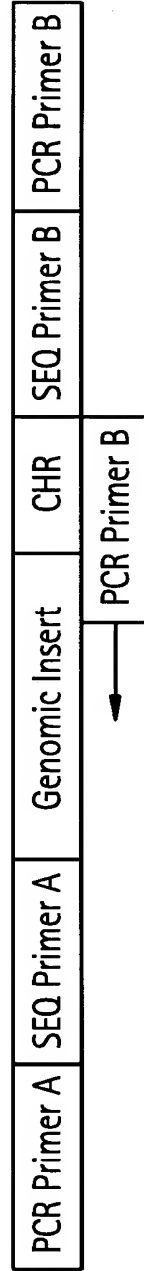


FIG. 27

Primer Candidates by T<sub>m</sub>  
8x19x19x19x9 tetrads (493,848 total possibilities)

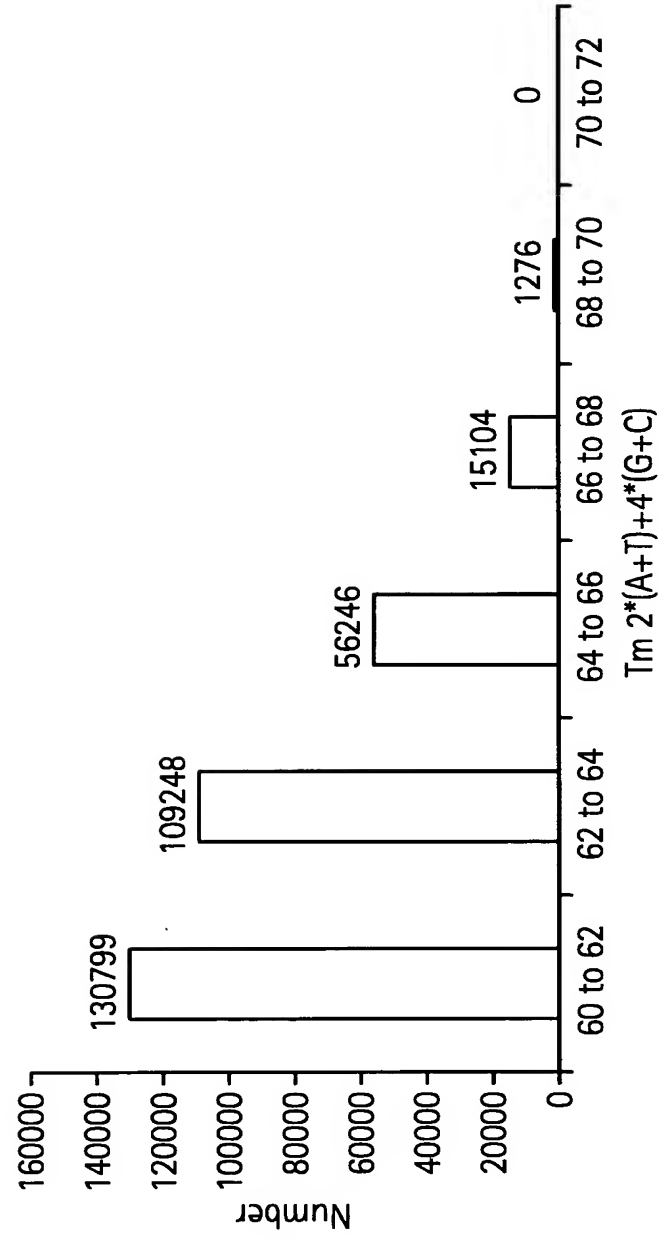


FIG. 28A



FIG. 28B



FIG. 28C

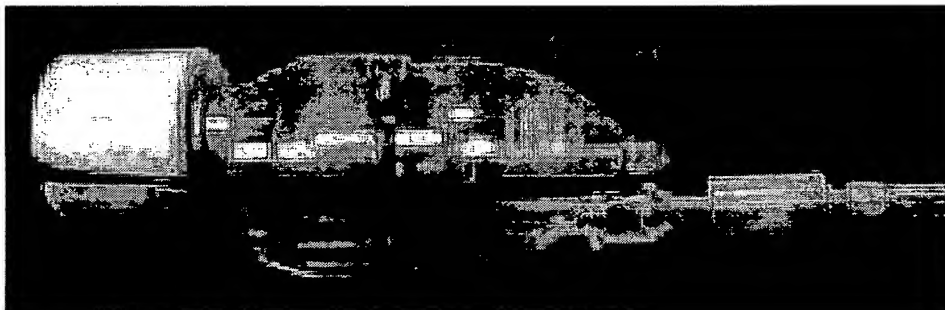


FIG. 28D

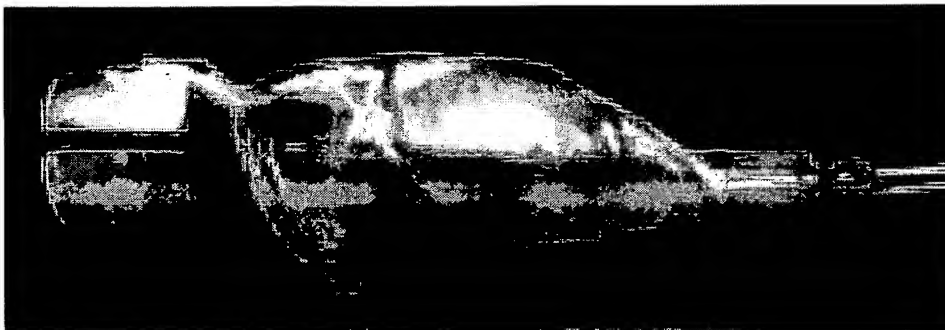


FIG. 29A

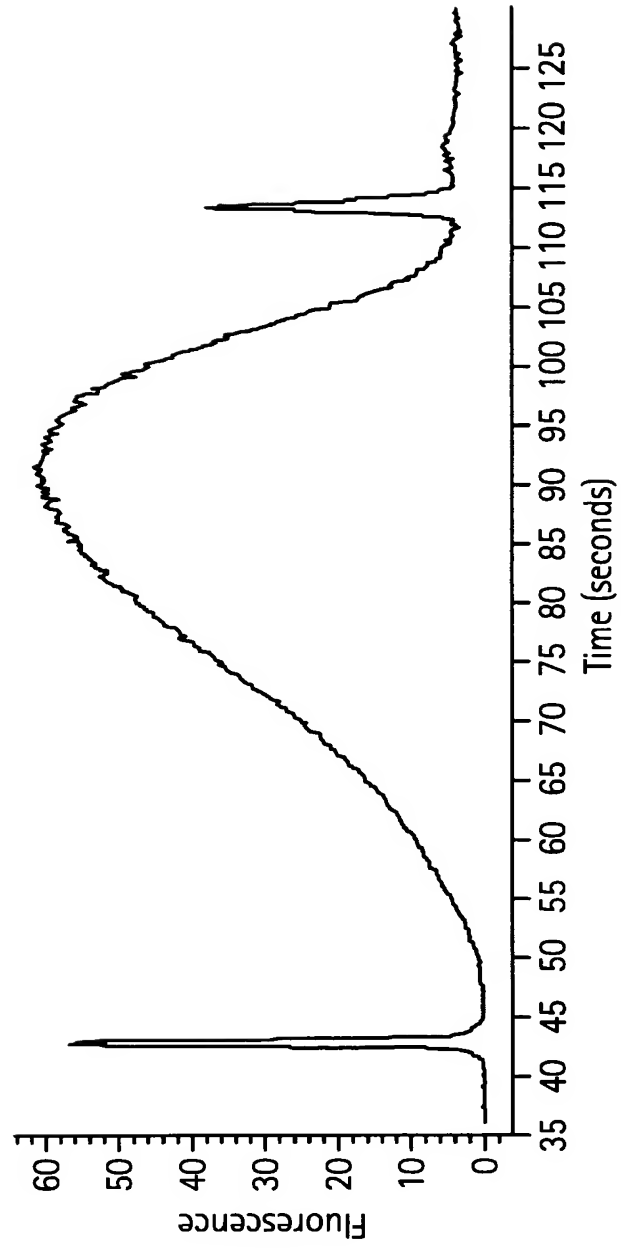


FIG. 29B

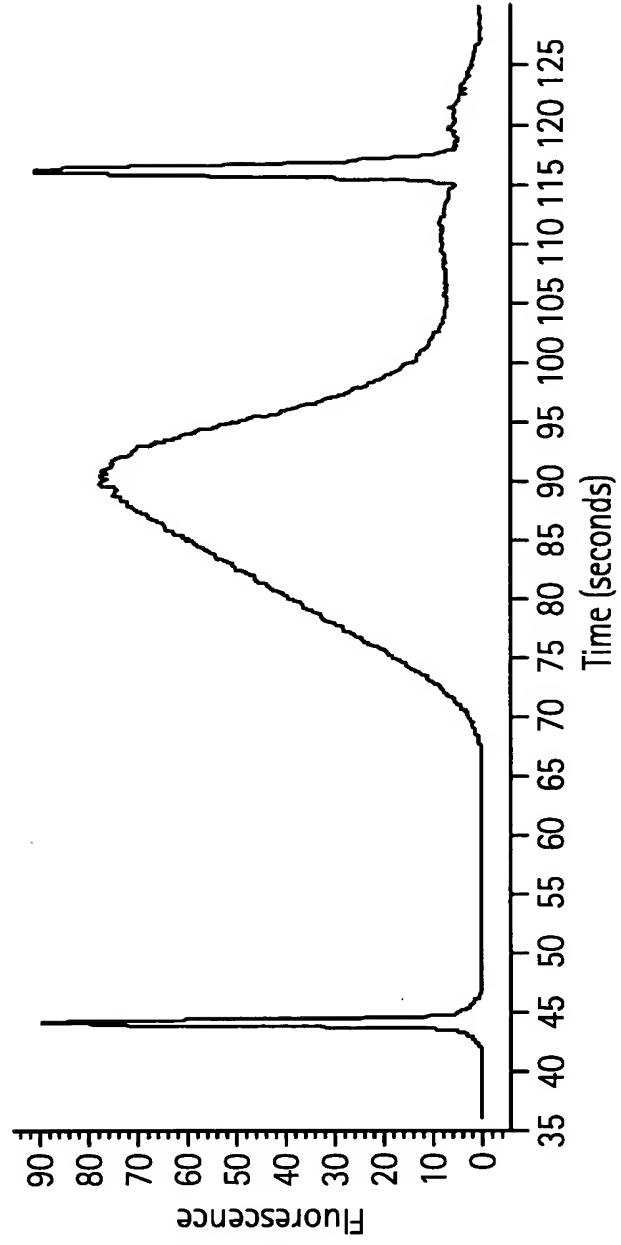




FIG. 30

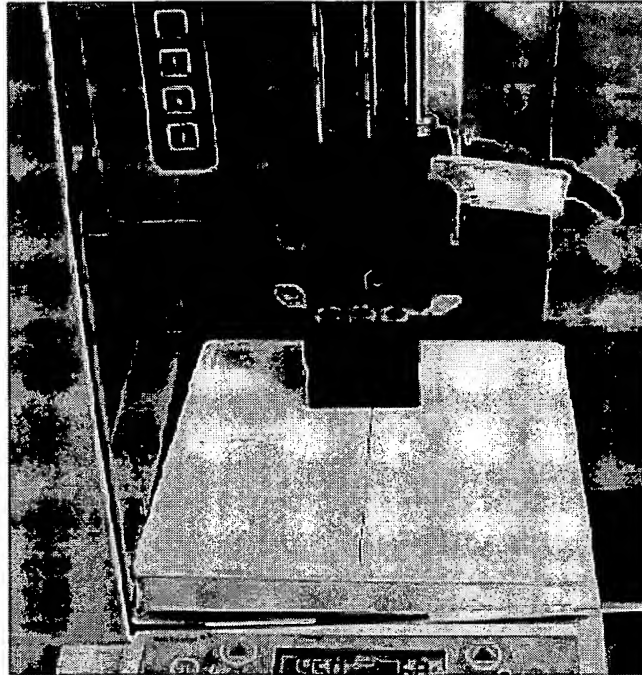


FIG. 31

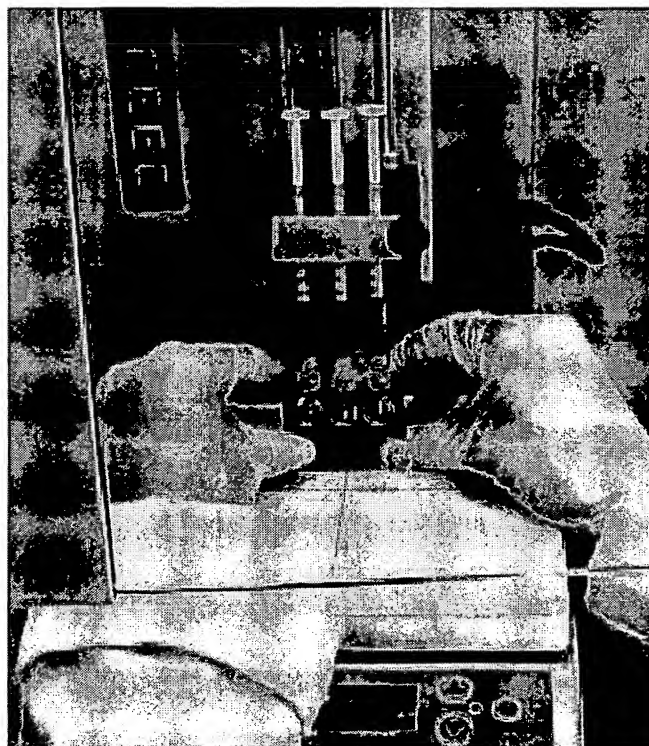


FIG. 32

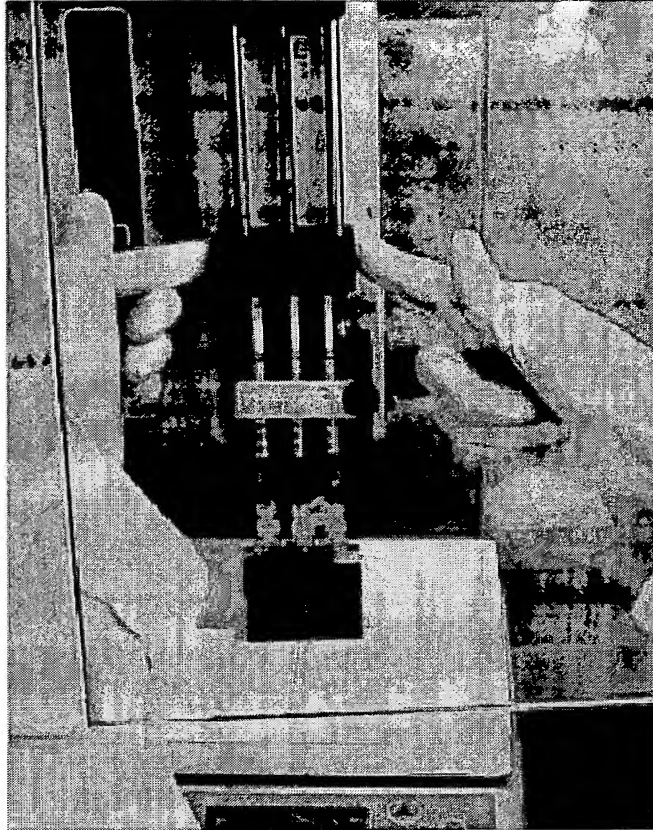


FIG. 33

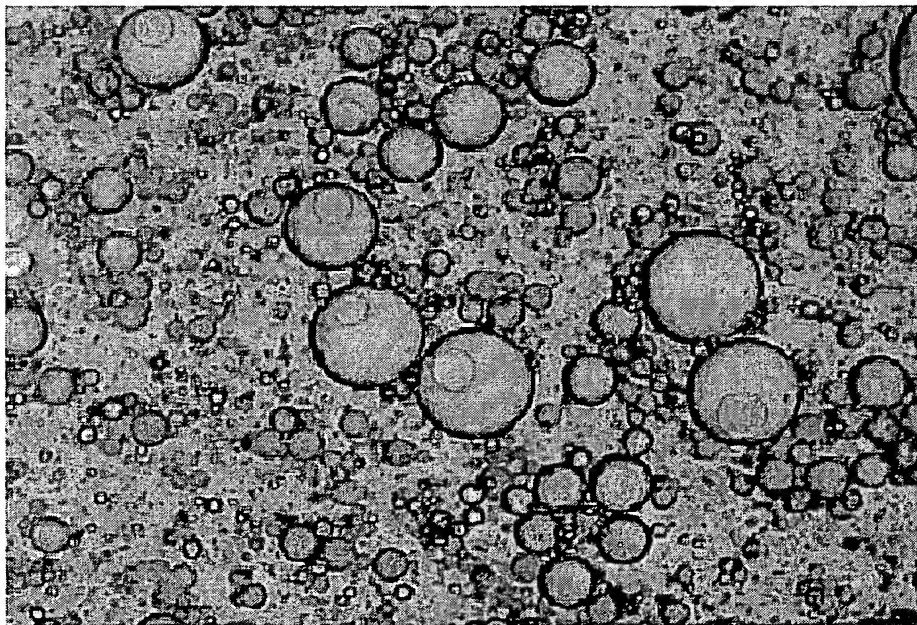
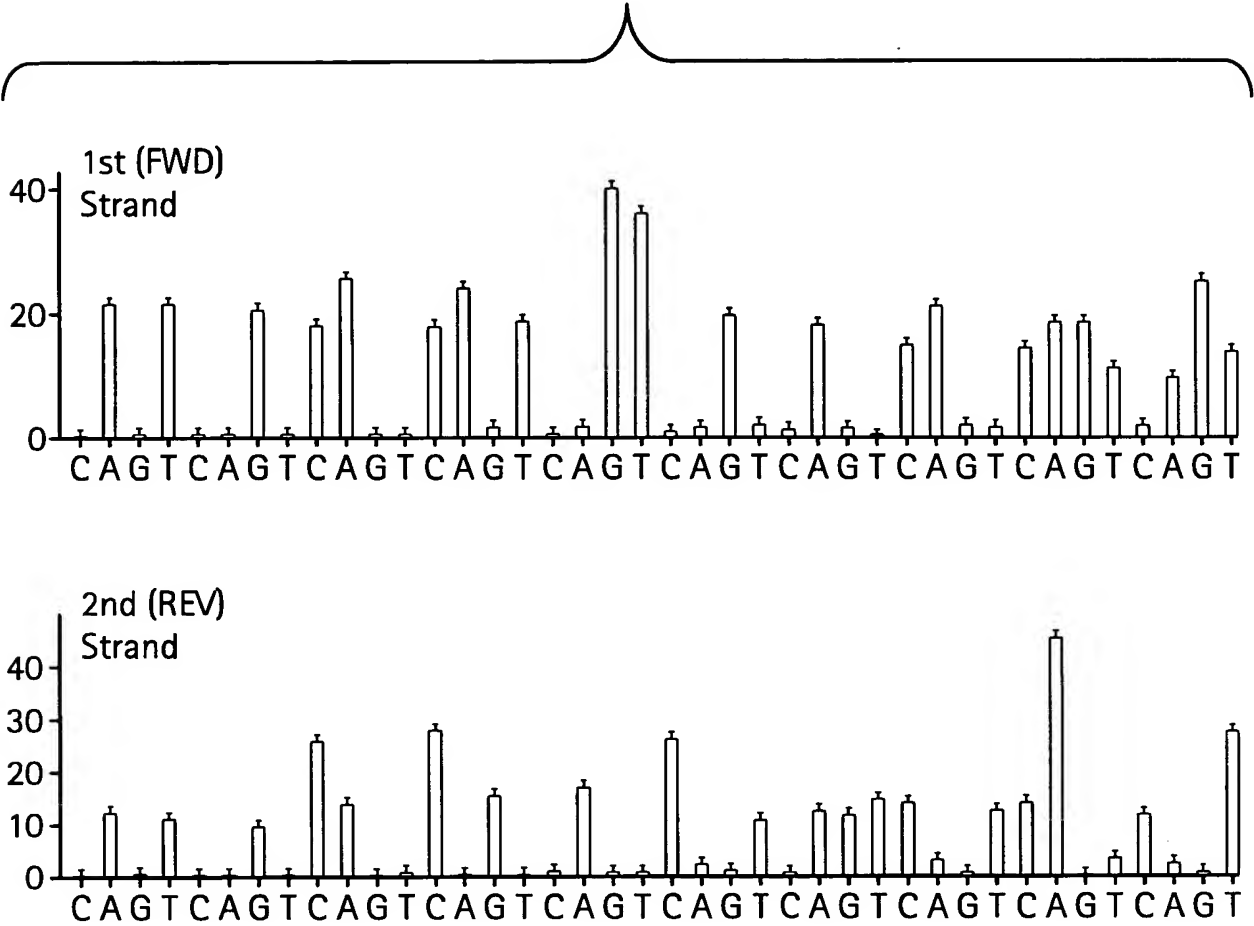


FIG. 34



1st Strand  
(FWD)

| Sample  | Well Location        | Sequence                | Perfect Match Length |
|---------|----------------------|-------------------------|----------------------|
| F6_14_1 | 00001_1362_1660.well | ATGCACATGGTTGACACAGTGGT | 22                   |

ATGC ACATGGTTGACACAGTGG

2nd Strand  
(REV)

| Sample  | Well Location        | Sequence                  | Perfect Match Length |
|---------|----------------------|---------------------------|----------------------|
| F6_14_1 | 00003_1363_1660.well | ATGCCACCGACCTAGTCTCAAACCT | 25                   |

ATGC CACCGACCTAGTCTCAAACCT

FIG. 35A



FIG. 35B

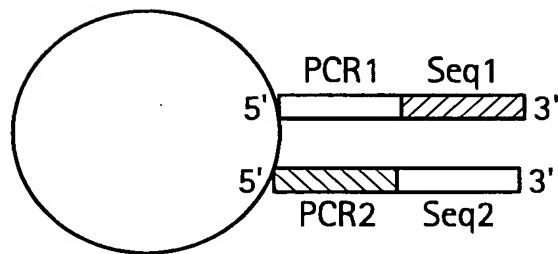


FIG. 35C

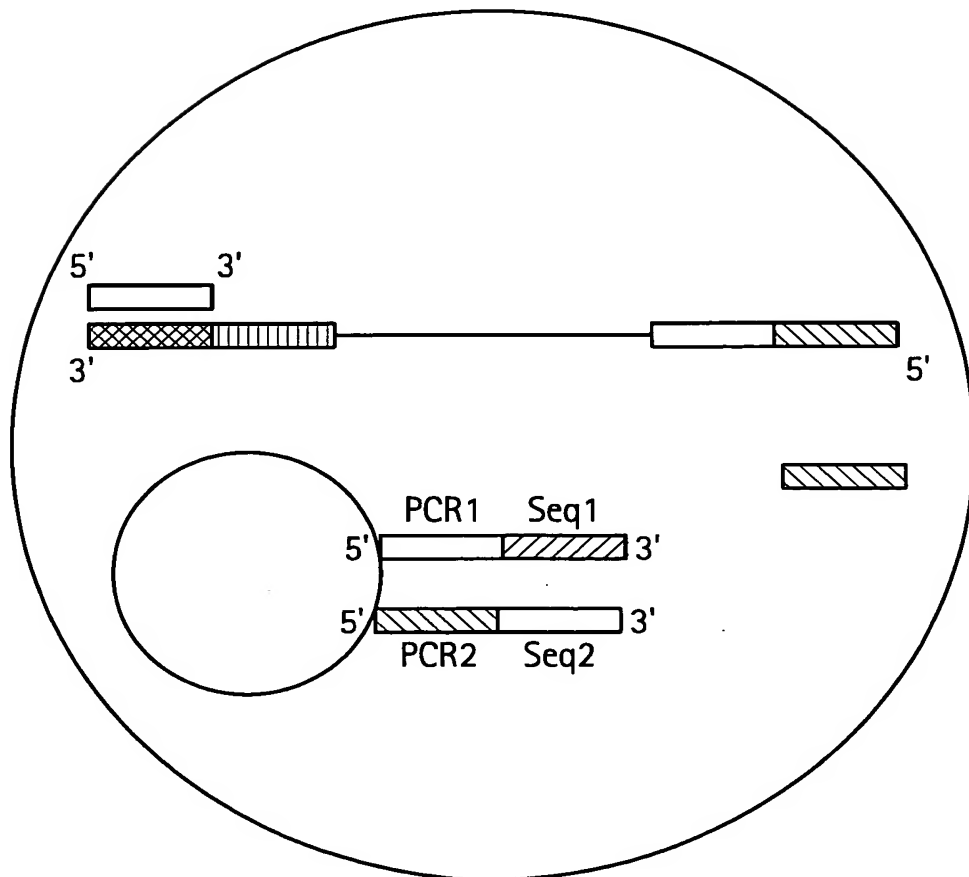


FIG. 36

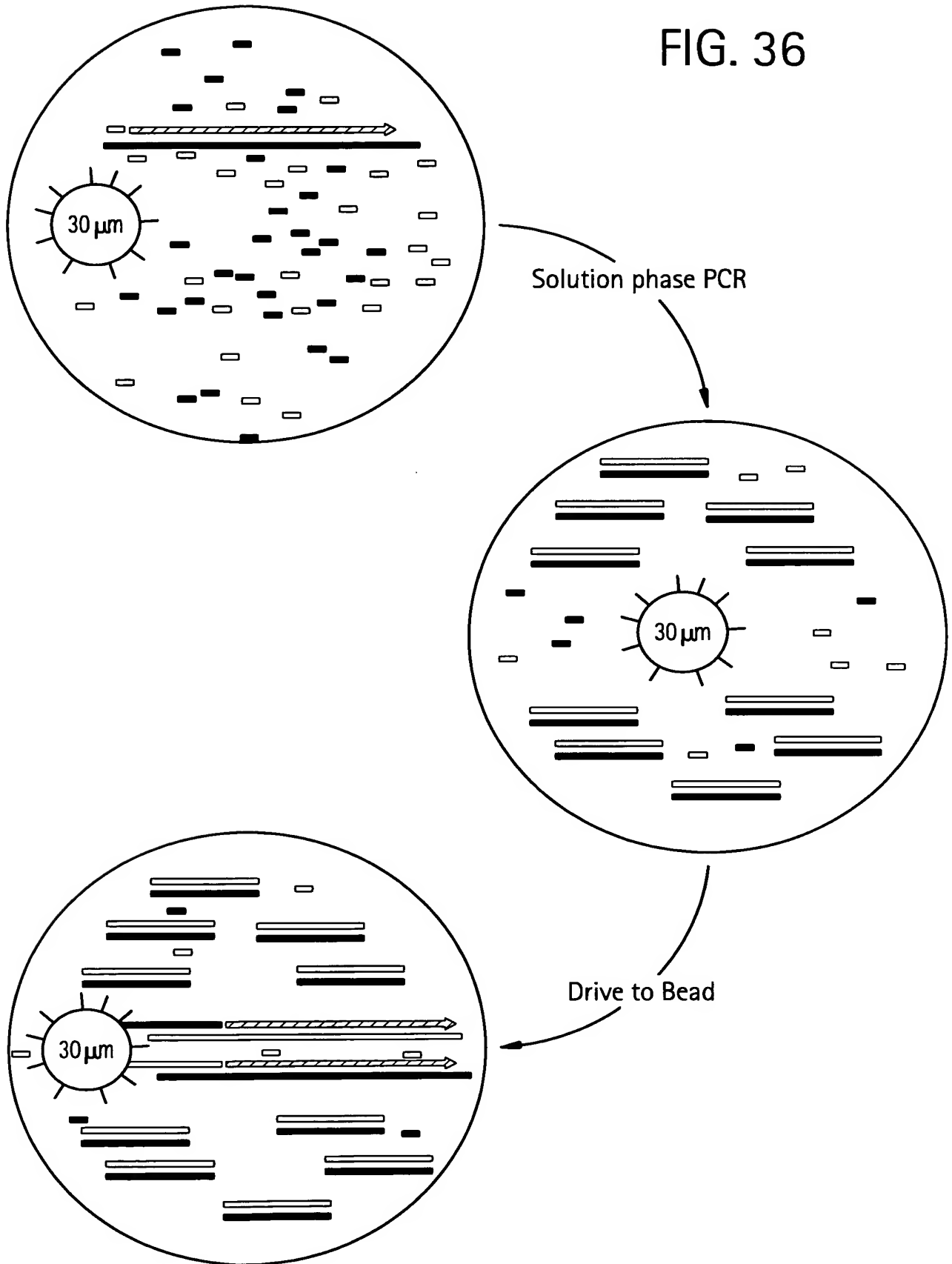
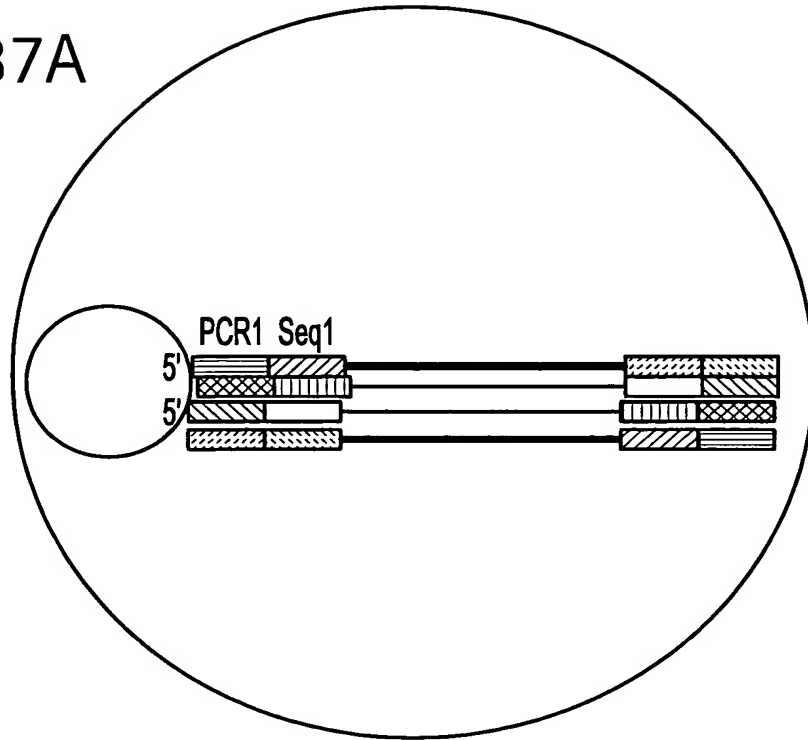


FIG. 37A



Emulsion breaking

FIG. 37B

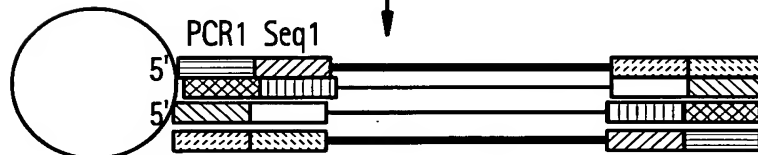
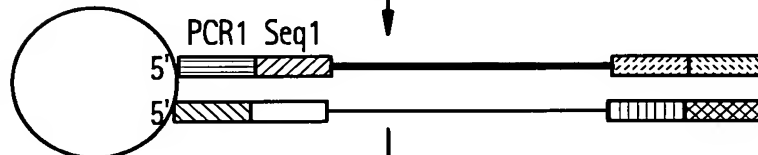
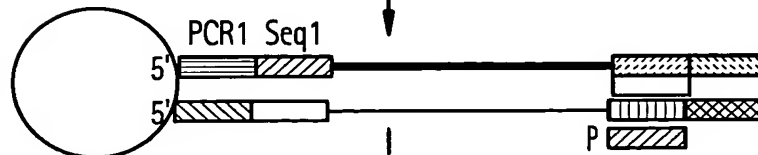
2nd strand removal and  
enrichment

FIG. 37C



Annealing sequencing primers

FIG. 37D



1st segment sequencing

FIG. 37E

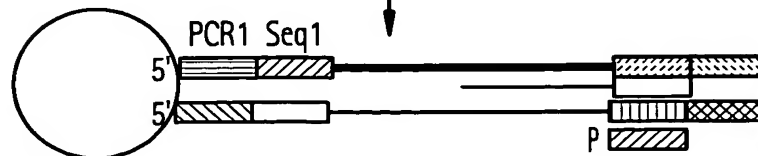


FIG. 38

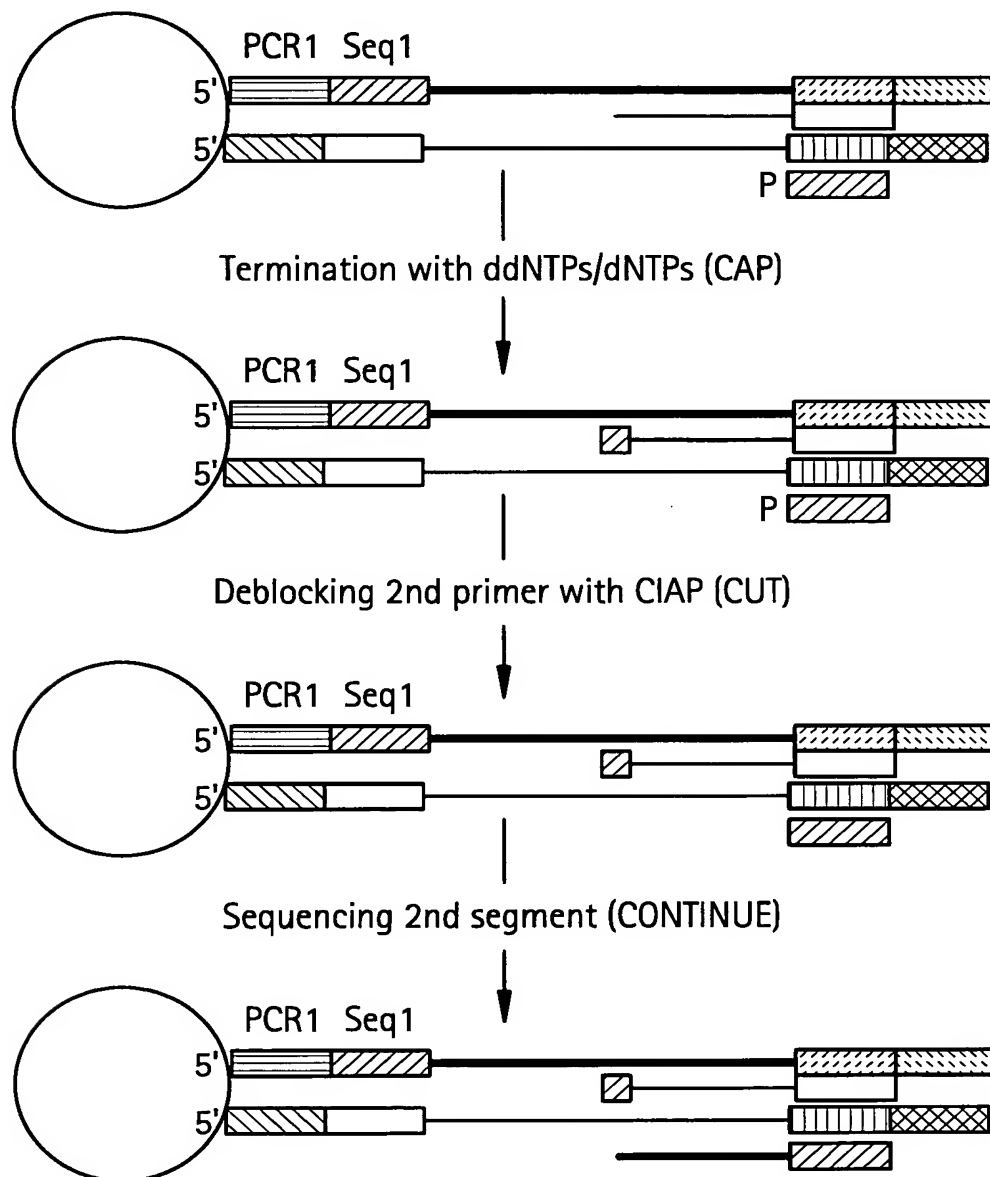


FIG. 39A

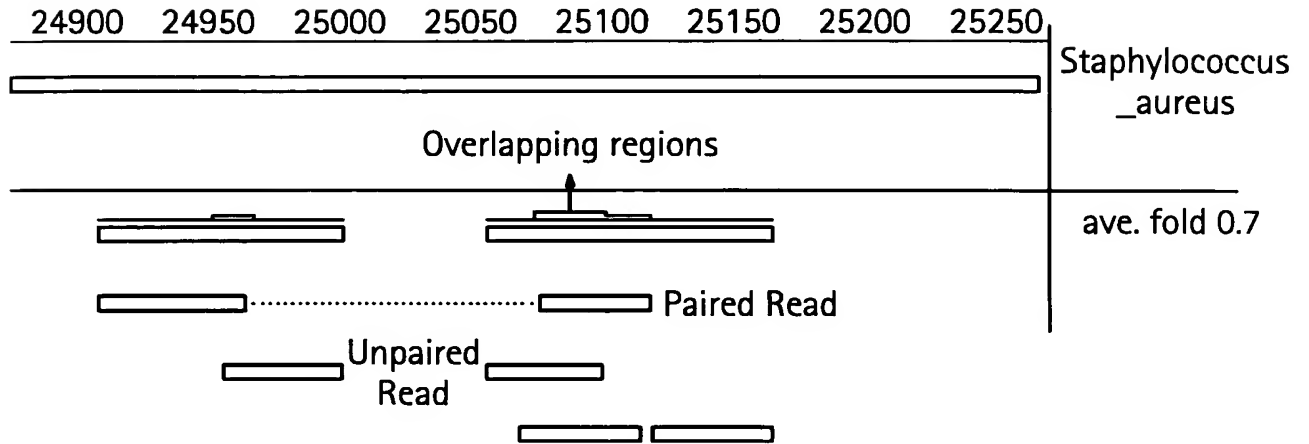


FIG. 39B

|                  |        |
|------------------|--------|
| Total Reads      | 31,785 |
| Total 1st Strand | 15,770 |
| Total 2nd Strand | 16,015 |
|                  |        |
| Paired           | 11,799 |
| Non Paired Reads | 8,187  |
| Total Coverage   | 38%    |

FIG. 40

Average 95±9 bases

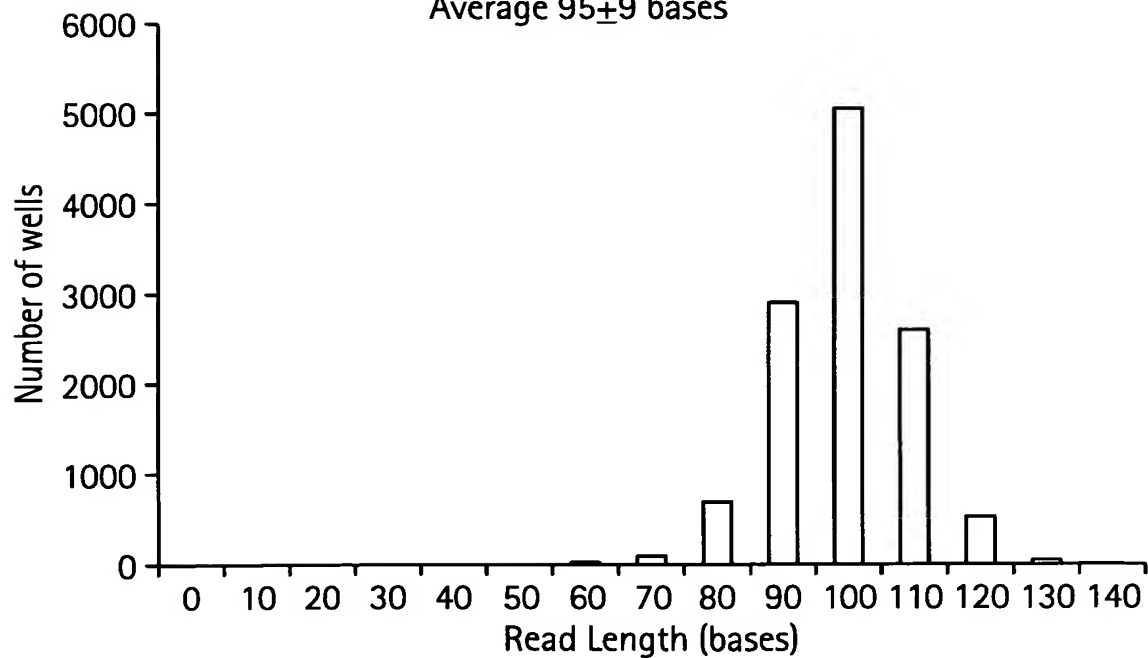




FIG. 41

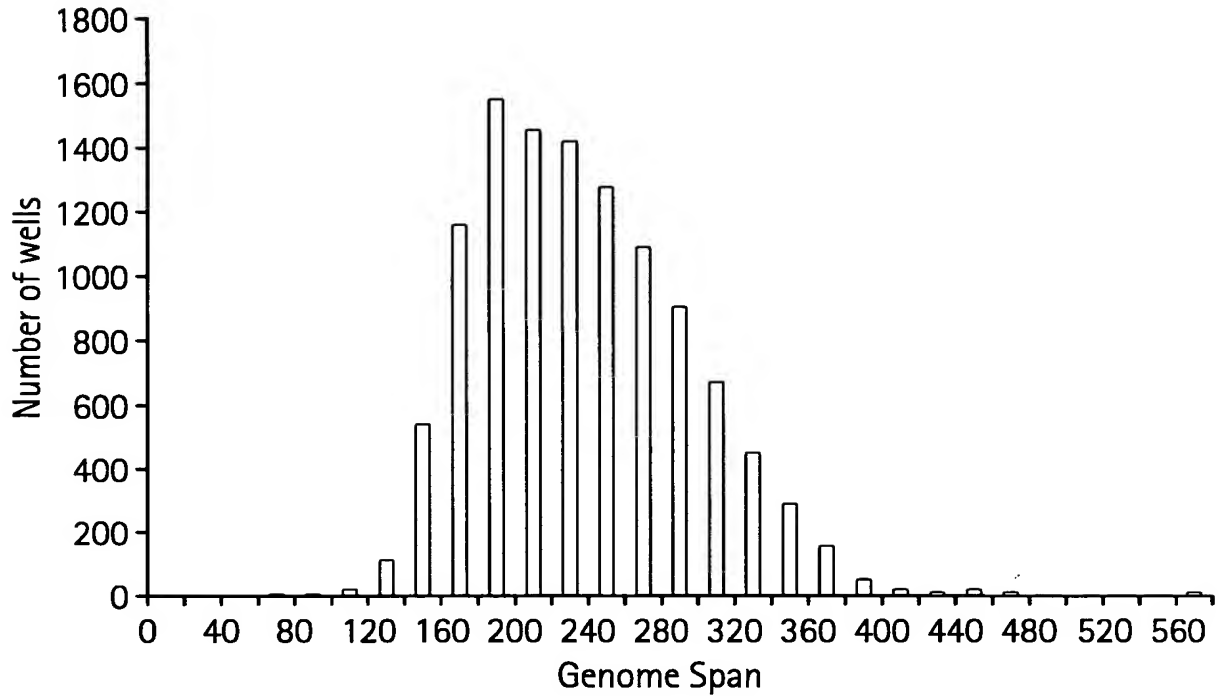


FIG. 42

| Well               | Genome Position | Orientation | Alignment String                                    |
|--------------------|-----------------|-------------|---|
| 00364_0548_2509    | 571366          | F           | TATTGTTGATGCTGTAAAAaGAAGCTACTGGTGTAGtATTTTTATGAAGTT |
| 00364_0548_2509_D2 | 571512          | R           | TGCTCAAAGAATTCATTTAAAAATATGACCATATTTCAITGTATCTTT    |
| 00383_0985_2232    | 1487890         | R           | AAGCGAACAGTCAAGTACCACAGTCAGTTGACtTTTACACAAGCGGAT    |
| 00383_0985_2232_D2 | 1487769         | F           | TACAGGTGTTGGTATGCCATTTGCGATTGTTGCGCTTGGTTAGCCG      |
| 00397_0940_2923    | 2611033         | F           | AACATATAAACATCCCCTATCTCAATTTCCGCTTCATGTaCAAAAAAAGC  |
| 00397_0940_2923_D2 | 2611164         | R           | TAGATATCACTTGCGTGTTACTGGTAATGCAGGCATGAG             |
| 00417_0611_1933    | 122001          | R           | ATCAACTCTGGAAATGCtTCTTGATACGCCTCGATGATG             |
| 00417_0611_1933_D2 | 121930          | F           | GATGAGGAGCTGCAATGGCAATGGGTAAAGGCATCATCG             |
| 00434_0595_0993    | 2022591         | R           | TGTATCTCGATTGGATTAGTTGCTTTTTGCATCTTCATTAGACC        |
| 00434_0595_0993_D2 | 2022473         | F           | CATTAACATCTGCACCAGAAATAGCTTCTAATACGATTGC            |
| 00443_1003_0754    | 107373          | F           | GCGACGACGTCCAGCTAATAACGCTGCACCTAAGGCTAATGATAAT      |
| 00443_1003_0754_D2 | 107502          | R           | AAACCATGCAGATGCTAACAAAGCTCAAGCATTACCAGAACT          |
| 00454_1257_3047    | 59038           | R           | TGTTGCTGCATCATAATTAATACTACATCATTTAAatCTTTGG         |
| 00454_1257_3047_D2 | 58880           | F           | GCAGATGGTGTGACTAACCAAGTTGGTCAAAATGCCCTAAATACAAAAGAT |